SEQUENCE LISTING

(1) GENERA	AL INFORMATION:
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- (i) APPLICANT: JONATHAN EDWARD LIGHTNER JOHN JOSEPH OKULEY
- (ii) TITLE OF INVENTION: GENES FOR MICROSOMAL FATTY ACID DELTA-12 DESATURASES AND RELATED ENZYMES FROM PLANTS
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
 - STREET: 1007 MARKET STREET (B)
 - (C)
 - CITY: WILMINGTON STATE: DELAWARE (D)
 - COUNTRY: U.S.A. (E)
 - (F) ZIP: 19898
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: MacIntosh
 - (C) OPERATING SYSTEM: MacIntosh 6.0
 - SOFTWARE: Microsoft Word 4.0 (D)
- CURRENT APPLICATION DATA: (vi)
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: U.S. 07/977,339
 - FILING DATE: 17-NOV-1992 (B)
- ATTORNEY/AGENT INFORMATION: (viii)
 - (A) NAME: Siegell, Barbara C.
 - (B) REGISTRATION NUMBER: 30,684
 - (C) REFERENCE/DOCKET NUMBER: BB-1043-B
 - TELECOMMUNICATION INFORMATION: (ix)
 - (A) TELEPHONE: (302) 992-4927 (B) TELEFAX: (302) 892-7949

 - (C) TELEX: 835420

(2) INFORMATION FOR SEQ ID NO:1:

			(i)	(A) (B) (C)		NGT PE:	H: ni DEDN	137 icle JESS	2 baic a	ase acid doub	pai:	rs			
			(ii	L)	MOL	ECUL	E T	YPE:	c	DNA						
			(iii	_)	HYPO	OTHE	TIC	AL:	NO							
			(iv	7)	ANT	I-SE	NSE	: N	0							
			(vi	.)	ORIC	SINA OR				rabi	idop	sis	tha	lia	na	
			(vii	.)	IMME (B)	EDIA CL		SOUR p		03						
			(ix	:)		URE NA LO	ME/I	KEY:			244					
			(xi	.)	SEQU	JENC	E DE	ESCR	IPT	ION:	S	EQ I	D N	0:1:		
AGA	GAGA	GAG .	ATTC'	TGCG	GA G	GAGC'	TTCT'	T CT	TCGT.	aggg	TGT	TCAT	CGT	TATT	AACGTT	60
ATC	GCCC	CTA (CGTC.	AGCT	CC A	TCTC	CAGA	A AC		Gly				Arg	ATG ' Met	113
CCG Pro	GTT Val	CCT Pro 10	ACT Thr	TCT Ser	TCC Ser	AAG Lys	AAA Lys 15	TCG Ser	GAA Glu	ACC Thr	GAC Asp	ACC Thr 20	ACA Thr	AAG Lys	CGT Arg	161
														AAA Lys	GCA Ala	209
														TCC Ser		257
														GCC Ala 70		305
AAT Asn	TAC Tyr	TTC Phe	TCT Ser 75	CTC Leu	CTC Leu	CCT Pro	CAG Gln	CCT Pro 80	CTC Leu	TCT Ser	TAC Tyr	TTG Leu	GCT Ala 85	TGG Trp	CCA Pro	353
														GTC Val		401

						TGG Trp		449
						CCT Pro		497
						GGA Gly		545
						ATC Ile 165	TGG Trp	593
						ATG Met		641
						AAC Asn		689
						AAC Asn		737
						GAT Asp	GGT Gly	785
						GCA Ala 245		833
						ATA Ile		881
						CCC Pro		929
						GCT Ala		977
						CAC His		1025
						CCG Pro 325		1073

Asn	GCA Ala												GGA Gly				1121
	CAG Gln 345																1169
	GAG Glu																1217
	TAC Tyr							TGAG	CATG	AT G	GTGA	AGAA	A TI	GTC	SACCT	•	1271
TTCT	CTTG	STC I	GTTI	GTCT	т тт	GTTA	AAGA	AGC	TATG	CTT	CGTI	TTAA	TA A	TCTI	TATTG	T	1331
CCAT	TTTG	STT G	TGTI	ATGA	C AT	TTTG	GCTG	CTC	ATTA	TGT	T						1372
	(2)	I	NFO	RMAT	ION	FOF	SE	QII	ON O	:2:							
			(i)	() ()	QUE A) B)	LEN TYP	CHA GTH: E: OLOC	: 3 ami	83 a	amin	o a	cids	3				
		(ii)	MC	LEC	ULE	TYP	E:	pro	tei	n						
		(xi)	SE	QUE	NCE	DES	CRIE	PTIO	N:	SEÇ) ID	NO:	2:		•	
	Met 1	Gly	·									•			Lys 15	Ser	
	1	Gly	Ala	Gly	Gly 5	Arg	Met	Pro	Val	Pro 10	Thr	Ser	Ser	Lys			
	1 Glu	Gly	Ala	Gly Thr 20	Gly 5 Thr	Arg Lys	Met Arg	Pro Val	Val Pro 25	Pro 10 Cys	Thr	Ser	Ser	Lys Pro 30	15	Ser	
	1 Glu Val	Gly Thr	Ala Asp Asp 35	Gly Thr 20	Gly 5 Thr Lys	Arg Lys	Met Arg Ala	Pro Val Ile 40	Pro 25	Pro 10 Cys	Thr Glu His	Ser Lys Cys	Ser Pro	Lys Pro 30 Lys	15 Phe	Ser	
	1 Glu Val Ile	Gly Thr Gly Pro 50	Ala Asp Asp 35	Gly Thr 20 Leu Ser	Gly 5 Thr Lys	Arg Lys Lys Ser	Met Arg Ala Tyr 55	Pro Val Ile 40 Leu	Val Pro 25 Pro	Pro 10 Cys Pro	Thr Glu His	Ser Lys Cys Ile 60	Ser Pro Phe 45	Pro 30 Lys	15 Phe Arg	Ser Ser	
	Glu Val Ile Cys 65	Gly Thr Gly Pro 50	Ala Asp Asp 35 Arg	Thr 20 Leu Ser	Gly 5 Thr Lys Phe Val	Arg Lys Lys Ser Ala 70	Met Arg Ala Tyr 55 Thr	Pro Val Ile 40 Leu Asn	Val Pro 25 Pro Ile	Pro 10 Cys Pro Ser	Thr Glu His Asp Ser 75	Lys Cys Ile 60	Pro Phe 45 Ile	Lys Pro 30 Lys Ile	15 Phe Arg Ala	Ser Ser Ser	
	Glu Val Ile Cys 65	Gly Thr Gly Pro 50 Phe	Ala Asp Asp 35 Arg	Thr 20 Leu Ser Tyr	Gly 5 Thr Lys Phe Val	Lys Lys Ser Ala 70	Met Arg Ala Tyr 55 Thr	Pro Val Ile 40 Leu Asn	Val Pro 25 Pro Ile Tyr	Pro 10 Cys Pro Ser Phe	Thr Glu His Asp Ser 75 Ala	Lys Cys Ile 60 Leu Cys	Pro Phe 45 Ile Leu Gln	Lys Pro 30 Lys Ile Pro	15 Phe Arg Ala Gln	Ser Ser Pro 80 Val	
	I Glu Val Ile Cys 65 Leu Leu	Gly Thr Gly Pro 50 Phe Ser	Ala Asp Asp 35 Arg Tyr	Thr 20 Leu Ser Tyr Leu	Gly 5 Thr Lys Phe Val Ala 85 Trp	Lys Lys Ser Ala 70 Trp	Met Arg Ala Tyr 55 Thr	Pro Val Ile 40 Leu Asn Leu Ala	Val Pro 25 Pro Ile Tyr Tyr His 105	Pro 10 Cys Pro Ser Phe	Thr Glu His Asp Ser 75 Ala	Lys Cys Ile 60 Leu Cys	Ser Pro Phe 45 Ile Leu Gln His	Lys Pro 30 Lys Ile Pro Gly His	15 Phe Arg Ala Gln Cys 95	Ser Ser Pro 80 Val	

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp 275 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu 295 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu 370 375

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

			(111	.,	III O	11111	. TCA.		NO								
			(iv	r) A	ITN.	-SEN	SE:	NC)								
			(vi	•	RIG (A)		SOI		E: Br	ass:	ica	nap	us				
			(vii		MMEI (B)					1651)						
			(i>	, (EATU (A) (B)	NAM	Æ/K		CD 99	-	250						
			(xi	L) S	EQU	ENCE	DE	SCRI	PTI	ON:	SE	Q II	O NC	:3:			
GAG	AGGA	GAC	AGAG	ACAG	AG A	GAGA	GTTG	A GA	GAGC	TCTC	GTA	GGTT	ATC	GTAT	TAACGI	?	60
AAT	CTTC	AAT	cccc	CCTA	CG T	CAGC	CAGC	T CA	AGAA					GT G ly G			113
					CCT Pro												161
				Cys	GAG Glu										AAG Lys		209
					CAC His												257
					GAC Asp												305
					CCT Pro 75										GCC Ala 85		353
TGG Trp	CCT Pro	CTC Leu	TAC Tyr	TGG Trp 90	GCC Ala	TGC Cys	CAG Gln	GGC Gly	TGC Cys 95	GTC Val	CTA Leu	ACC Thr	GGC Gly	GTC Val 100	TGG Trp		401
					TGC Cys												449
CTG Leu	GAC Asp	GAC Asp 120	ACC Thr	GTC Val	GGC Gly	CTC Leu	ATC Ile 125	TTC Phe	CAC His	TCC Ser	TTC Phe	CTC Leu 130	CTC Leu	GTC Val	CCT Pro		497

TAC Tyr	TTC Phe 135	TCC Ser	TGG Trp	AA G Lys	TAC Tyr	AGT Ser 140	CAT His	CGA Arg	CGC Arg	CAC His	CAT His 145	Ser	AAC Asn	ACT Thr	GGC Gly	545
TCC Ser 150	CTC Leu	GAG Glu	AGA Arg	GAC Asp	GAA Glu 155	GTG Val	TTT Phe	GTC Val	CCA Pro	AGA Arg 160	AGA Arg	AGT Ser	CAG Gln	ACA Thr	TCA Ser 165	593
			GCA Ala													641
			TTC Phe 185													689
			CCT Pro													737
			TAC Tyr													785
			CTC Leu													833
CAA Gln	GGA Gly	GTT Val	GCC Ala	TCG Ser 250	ATG Met	GTC Val	TGC Cys	TTC Phe	CTA Leu 255	CGA Arg	GTT Val	CCT Pro	CTT Leu	CTG Leu 260	ATT Ile	881
			TTC Phe 265													929
TCC Ser	CTG Leu	CCT Pro 280	CAC His	TAT Tyr	GAC Asp	TCG Ser	TCT Ser 285	GAG Glu	TGG Trp	GAT Asp	TGG Trp	TTG Leu 290	AGG Arg	GGA Gly	GCT Ala	977
			GTT Val													1025
AAT Asn 310	ATC Ile	ACG Thr	GAC Asp	ACG Thr	CAC His 315	GAG Glu	GCG Ala	CAT His	CAC His	CTG Leu 320	TTC Phe	TCG Ser	ACC Thr	ATG Met	CCG Pro 325	1073
CAT Hiq	TAT Tyr	CAT His	GCG Ala	ATG Met 330	GAA Glu	GCT Ala	ACG Thr	AAG Lys	GCG Ala 335	ATA Ile	AA G	CCG Pro	ATA Ile	CTG Leu 340	GGA Gly	1121
G A G Glu	TAT Tyr	TAT Tyr	CAG Gln 345	TTC Phe	GAT Asp	GGG Gly	ACG Thr	CCG Pro 350	GTG Val	GTT Val	AAG Lys	Ala	ATG Met 355	TGG Trp	AGG Arg	1169

	GCG Ala																1217
	GGT Gly 375									TGA	\GCA#	AG A	AGA#	ACTO	βA		1267
ACCI	TTCT	CT T	CTAT	CAAT	T GT	CTTT	GTTT	' AAG	AAGC	TAT	GTTI	CTGI	TT C	CAATA	ATCI	T.	1327
AATI	ATCC	AT T	TTGT	TGTG	т тт	TCTG	ACAT	TTT	'GGC'I	'AAA	ATTA	TGTO	AT G	TTGG	AAGT	T	1387
AGTG	TCT																1394
	(2)	I	NFO	RMAT	ION	FOR	SE	QII) NO	:4:							
		,	(i)	(A) (B) (D)) I) I) I	ENG YPE OPO	TH: : & LOGY	ACTE 38 amin (:	3 ar o ac line	minc cid ear	S: ac	ids					
								RIPI			SEO	TD 1	NO : 4	l <u>.</u>			
	Met 1														Lys 15	Ser	
		Thr	Asp	Asn 20		Lys	Arg	Val	Pro 25		Glu	Thr	Pro	Pro 30	Phe	Thr	
	Val	Gly	Glu 35	Leu	Lys	Lys	Ala	Ile 40	Pro	Pro	His	Cys	Phe 45	Lys	Arg	Ser	
	Ile	Pro 50	Arg	Ser	Phe	Ser	ніs 55	Leu	Ile	Trp	Asp	Ile 60	Ile	Ile	Ala	Ser	
	Cys 65	Phe	Tyr	Tyr	Val	Ala 70	Thr	Thr	Tyr	Phe	Pro 75	Leu	Leu	Pro	Asn	Pro 80	
	Leu	Ser	Tyr	Phe	Ala 85	Trp	Pro	Leu	Tyr	Trp 90	Ala	Суз	Gln	Gly	Суз 95	Val	
	Leu	Thr	Gly	Val 100	Trp	Val	Ile	Ala	His 105	Glu	Суз	Gly	His	Ala 110	Ala	Phe	
	Ser	Asp	Tyr 115	Gln	Trp	Leu	Asp	Asp 120	Thr	Val	Gly	Leu	Ile 125	Phe	His	Ser	
	Phe	Leu 130	Leu	Val	Pro	Tyr	Phe 135	Ser	Trp	Lys	Tyr	Ser 140	His	Arg	Arg	His	
	His 145	Ser	Asn	Thr	Gly	Ser 150	Leu	Glu	Arg	Asp	Glu 155	Val	Phe	Val	Pro	Arg 160	
	Arg	Ser	Gln	Thr	Ser 165	Ser	Gly	Thr	Ala	Ser 170	Thr	Ser	Thr	Thr	Phe 175	Gly	

Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu Tyr 180 Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln 215 Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Leu Pro Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Leu Arg Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu 295 Asn Gln Gly Phe His Asn Ile Thr Asp Thr His Glu Ala His His Leu 305 Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Glycine max

(vii) IMMEDIATE SOURCE:

			(• = =	- /		CI				-165	5K					
			(ix	()	FEA: (A) (B)		ME/	KEY:		DS 08	. 124	7				
			(xi	.)	SEQU	JENC	E DI	ESCR	IPT	ION:	s	EQ :	ED N	0:5	:	
CCA	TATA	CTA	ATAT	TTGC	TT G	TATT	GATA	G CC	CCTC	CGTT	ccc	AAGA	GTA	TAAA	ACTGCA	60
TCG.	AATA.	ATA ·	CAAG	CCAC	TA G	GCAT	GGGT	C TA	GCAA.	AGGA	AAC	AACA			GGT Gly	116
AGA Arg	GGT Gly 5	Arg	GTG Val	GCC Ala	AAA Lys	GTG Val 10	GAA Glu	GTT Val	CAA Gln	GGG Gly	AAG Lys 15	Lys	CCT Pro	CTC Leu	TCA Ser	164
						CCA Pro										212
GCA Ala	ATT Ile	CCA Pro	CCA Pro	CAC His 40	TGC Cys	TTT Phe	CAG Gln	CGC A rg	TCC Ser 45	CTC Leu	CTC Leu	ACT Thr	TCA Ser	TTC Phe 50	TCC Ser	260
TAT Tyr	GTT Val	GTT Val	TAT Tyr 55	GAC Asp	CTT Leu	TCA Ser	TTT Phe	GCC Ala 60	TTC Phe	ATT Ile	TTC Phe	TAC Tyr	ATT Ile 65	GCC Ala	ACC Thr	308
ACC Thr	TAC Tyr	TTC Phe 70	CAC	CTC Leu	CTT Leu	CCT Pro	CAA Gln 75	CCC Pro	TTT Phe	TCC Ser	CTC Leu	ATT Ile 80	GCA Ala	TGG Trp	CCA Pro	356
ATC Ile	TAT Tyr 85	TGG Trp	GTT Val	CTC Leu	CAA Gln	GGT Gly 90	TGC Cys	CTT Leu	CTC Leu	ACT Thr	GGT Gly 95	GTG Val	TGG Trp	GTG Val	ATT Ile	404
GCT Ala 100	CAC His	GAG Glu	TGT Cys	GGT Gly	CAC His 105	CAT His	GCC Ala	TTC Phe	AGC Ser	AAG Lys 110	TAC Tyr	CAA Gln	TGG Trp	GTT Val	GAT Asp 115	452
GAT Asp	GTT Val	GTG Val	GGT Gly	TTG Leu 120	ACC Thr	CTT Leu	CAC His	TCA Ser	ACA Thr 125	CTT Leu	TTA Leu	GTC Val	CCT Pro	TAT Tyr 130	TTC Phe	500
TCA Ser	TGG Trp	AAA Lys	ATA Ile 135	AGC Ser	CAT His	CGC Arg	CGC Arg	CAT His 140	CAC His	TCC Ser	AAC Asn	ACA Thr	GGT Gly 145	TCC Ser	CTT Leu	548
GAC Asp	CGT Arg	GAT. Asp 150	GAA Glu	GTG Val	TTT Phe	GTC Val	CCA Pro 155	AAA Lys	CCA Pro	AAA Lys	TCC Ser	AAA Lys 160	GTT Val	GCA Ala	TGG Trp	596

						AAC Asn 170										644
	Thr					TGG Trp										692
						TTT Phe										740
						AGG Arg										788
						TCT Ser										836
						GTT Val 250										884
						ACA Thr										932
						GAA Glu										980
						GGG Gly										1028
						CAC His										1076
						AAT Asn 330										1124
TAC Tyr 340	C AA Gln	TTT Phe	GAT Asp	GAC Asp	ACA Thr 345	CCA Pro	TTT Phe	TAC Tyr	AAG Lys	GCA Ala 350	CTG Leu	TGG Trp	AGA Arg	GAA Glu	GCG Ala 355	1172
						GAG Glu										1220
						AAG Lys		TGAT 380	'GGAG	CA A	CCAA	TGGG	C CA	TAGT	'GGGA	1274
GTTA	TGGA	AG I	TTTG	TCAT	G TA	TTAG	TACA	TAA	TTAG	TAG	AATG	TTAT	AA A	TAAG	TGGAT	1334

TTGCCGC	GTA A	ATGA	CTTTC	GT G	rgtai	TGTC	AA.	ACAG	CTTG	TTG	CGATO	CAT	GTT	ATAAT	rG
TAAAAAT	AAT :	CTG	STATI	ra ar	TACA	ATGTG	GA2	AAGTO	STTC	TGC	TAT	AGC 1	TTC	rgcci	ΓA
AAAAAA	Ą														
(2)) I	NFO	RMAI	CION	FOR	R SE	Q II	D NC	:6:						
		(i)	SE((A) (B) (D)	L	CE (ENGI YPE: OPOI	TH:	379 mino		ino id	S: aci	.ds				
	((ii)	MOI	LECU	LE :	TYPE	: ;	prot	ein						
	(xi)	SEC	QUEN	CE I	DESC	RIP'	TION	ī:	SEQ	ID	NO:	5:		
Met 1		Gly	Arg	Gly 5	Arg	Val	Ala	Lys	Val 10		Val	Gln	Gly	Lys 15	_
Pro	Leu	Ser	Arg 20	Val	Pro	Asn	Thr	Lys 25	Pro	Pro	Phe	Thr	Val 30	Gly	Gln
Leu	Lys	Lys 35	Ala	Ile	Pro	Pro	His 40	Суз	Phe	Gln	Arg	Ser 45	Leu	Leu	Thr
Ser	Phe 50		Tyr	Val	Val	Tyr 55	Asp	Leu	Ser	Phe	Ala 60	Phe	Ile	Phe	Tyr
Ile 65		Thr	Thr	Tyr	Phe 70	His	Leu	Leu	Pro	Gln 75	Pro	Phe	Ser	Leu	Ile 80
Ala	Trp	Pro	Ile	Туг 85	Trp	Val	Leu	Gln	Gly 90	Суз	Leu	Leu	Thr	Gly 95	Val
Trp	Val	Ile	Ala 100	His	Glu	Cys	Gly	His 105	His	Ala	Phe	Ser	Lys 110	Tyr	Gln
Trp	Val	Asp 115	Asp	Val	Val	Gly	Leu 120	Thr	Leu	His	Ser	Thr 125	Leu	Leu	Val
Pro	Tyr 130	Phe	Ser	Trp	Lys	Ile 135	Ser	His	Arg	Arg	His 140	His	Ser	Asn	Thr
Gly 1 4 5	Ser	Leu	Asp	Arg	Asp 150	Glu	Val	Phe	Val	Pro 155	Lys	Pro	Lys	Ser	Lys 160
Val	Ala	Trp	Phe	Ser 165	Lys	Tyr	Leu	Asn	Asn 170	Pro	Leu	Gly	Arg	Ala 175	Val
Ser	Leu	Leu	Val 180	Thr	Leu	Thr	Ile	Gly 185	Trp	Pro	Met	Tyr	Leu 190	Ala	Phe
Asn	Val	Ser 195	Gly	Arg	Pro	Tyr	Asp 200	Ser	Phe	Ala	Ser	His 205	Tyr	His	Pro

Tyr Ala Pro Ile Tyr Ser Asn Arg Glu Arg Leu Leu Ile Tyr Val Ser 210 215 220

Asp Val Ala Leu Phe Ser Val Thr Tyr Ser Leu Tyr Arg Val Ala Thr 225 230 235 240

Leu Lys Gly Leu Val Trp Leu Leu Cys Val Tyr Gly Val Pro Leu Leu 245 250 255

Ile Val Asn Gly Phe Leu Val Thr Ile Thr Tyr Leu Gln His Thr His 260 265 270

Phe Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly 275 280 285

Ala Leu Ala Thr Met Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe 290 295 300

His His Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr Met 305 310 315 320

Pro His Tyr His Ala Met Glu Ala Thr Asn Ala Ile Lys Pro Ile Leu 325 330 335

Gly Glu Tyr Tyr Gln Phe Asp Asp Thr Pro Phe Tyr Lys Ala Leu Trp 340 345 350

Arg Glu Ala Arg Glu Cys Leu Tyr Val Glu Pro Asp Glu Gly Thr Ser 355 360 365

Glu Lys Gly Val Tyr Trp Tyr Arg Asn Lys Tyr 370 375

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1790 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Zea mays
- (vii) IMMEDIATE SOURCE:
 (B) CLONE: pFad2#1
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 165..1328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7: CGGCCTCTCC CCTCCTCCT CCCTGCAAAT CCTGCAGACA CCACCGCTCG TTTTTCTCTC 60 CGGGACAGGA GAAAAGGGGA GAGAGAGGTG AGGCGCGGTG TCCGCCCGAT CTGCTCTGCC 120 CCGACGCAGC TGTTACGACC TCCTCAGTCT CAGTCAGGAG CAAG ATG GGT GCC GGC 176 Met Gly Ala Gly GGC AGG ATG ACC GAG AAG GAG CGG GAG AAG CAG GAG CTC GCC CGA 224 Gly Arg Met Thr Glu Lys Glu Arg Glu Lys Gln Glu Gln Leu Ala Arg GCT ACC GGT GGC GCC GCG ATG CAG CGG TCG CCG GTG GAG AAG CCT CCG 272 Ala Thr Gly Gly Ala Ala Met Gln Arg Ser Pro Val Glu Lys Pro Pro TTC ACT CTG GGT CAG ATC AAG AAG GCC ATC CCG CCA CAC TGC TTC GAG 320 Phe Thr Leu Gly Gln Ile Lys Lys Ala Ile Pro Pro His Cys Phe Glu CGC TCG GTG CTC AAG TCC TTC TCG TAC GTG GTC CAC GAC CTG GTG ATC 368 Arg Ser Val Leu Lys Ser Phe Ser Tyr Val Val His Asp Leu Val Ile GCC GCG GCG CTC CTC TAC TTC GCG CTG GCC ATC ATA CCG GCG CTC CCA 416 Ala Ala Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile Pro Ala Leu Pro 70 75 AGC CCG CTC CGC TAC GCC GCC TGG CCG CTG TAC TGG ATC GCG CAG GGG 464 Ser Pro Leu Arg Tyr Ala Ala Trp Pro Leu Tyr Trp Ile Ala Gln Gly 95 TGC GTG TGC ACC GGC GTG TGG GTC ATC GCG CAC GAG TGC GGC CAC CAC 512 Cys Val Cys Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His 105 110 GCC TTC TCG GAC TAC TCG CTC CTG GAC GAC GTG GTC GGC CTG GTG CTG 560 Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp Val Val Gly Leu Val Leu 125 CAC TCG TCG CTC ATG GTG CCC TAC TTC TCG TGG AAG TAC AGC CAC CGG 608 His Ser Ser Leu Met Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg 140 CGC CAC CAC TCC AAC ACG GGG TCC CTG GAG CGC GAC GAG GTG TTC GTG 656 Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val 155 CCC AAG AAG AAG GAG GCG CTG CCG TGG TAC ACC CCG TAC GTG TAC AAC 704

Pro Lys Lys Lys Glu Ala Leu Pro Trp Tyr Thr Pro Tyr Val Tyr Asn

AAC Asn	Pro	G GTC	GGC Gly	CGC Arg 185	y Val	G GTG	G CAC	C ATO	C GT(e Val 19(Va:	G CAC	G CTO	C ACC	CTC Let	C GGG u Gly 5	75	52
TGG Trp	CCG Pro	CTC Leu	TAC Tyr 200	Let	G GCC	ACC Thr	AAC Asr	GC0 Ala 205	a Ser	GG(G CGG 7 Arg	Pro	TAC Tyr 210	Pro	G CGC	80	0
TTC Phe	GCC	TGC Cys 215	HIS	TTC Phe	GAC Asp	CCC Pro	TAC Tyr 220	: Gl	C CCC	ATC Ile	TAC Tyr	AAC Asn 225	qeA	CGC Arc	G GAG g Glu	8 4	8
CGC Arg	GCC Ala 230	. Gin	ATC	TTC Phe	GTC Val	TCG Ser 235	GAC Asp	GCC Ala	GGC Gly	GTC Val	GTG Val 240	Ala	GTG Val	GCC Ala	TTC Phe	89	6
GGG Gly 245	CTG Leu	TAC	AAG Lys	CTG Leu	GCG Ala 250	GCG Ala	GCG Ala	TTC	GGG Gly	GTC Val 255	Trp	TGG Trp	GTG Val	GTG Val	CGC Arg 260	94	4
GTG Val	TAC Tyr	GCC Ala	GTG Val	CCG Pro 265	CTG Leu	CTG Leu	ATC Ile	GTG Val	AAC Asn 270	GCG Ala	TGG Trp	CTG Leu	GTG Val	CTC Leu 275	ATC	992	2
ACC Thr	TAC Tyr	CTG Leu	CAG Gln 280	CAC His	ACC Thr	CAC His	CCG Pro	TCG Ser 285	CTC Leu	CCC Pro	CAC His	TAC Tyr	GAC Asp 290	TCG Ser	AGC Ser	1040)
GAG Glu	TGG Trp	GAC Asp 295	TGG Trp	CTG Leu	CGC Arg	GGC Gly	GCG Ala 300	CTG Leu	GCC Ala	ACC Thr	ATG Met	GAC Asp 305	CGC Arg	GAC Asp	TAC Tyr	1088	3
GIY	ATC Ile 310	CTC Leu	AAC Asn	CGC Arg	GTG Val	TTC Phe 315	CAC His	AAC Asn	ATC Ile	ACG Thr	GAC Asp 320	ACG Thr	CAC His	GTC Val	GCG Ala	1136	5
CAC His 325	CAC His	CTC Leu	TTC Phe	TCC Ser	ACC Thr 330	ATG Met	CCG Pro	CAC His	TAC Tyr	CAC His 335	GCC Ala	ATG Met	GAG Glu	GCC Ala	ACC Thr 340	1184	
AAG (GCG Ala	ATC Ile	Arg	CCC Pro 345	ATC Ile	CTC Leu	GGC Gly	GAC Asp	TAC Tyr 350	TAC Tyr	CAC His	TTC Phe	qzA	CCG Pro 355	ACC Thr	1232	
CCT (GTC /	Ala	AAG Lys 360	GCG Ala	ACC Thr	TGG (Arg	GAG Glu 365	GCC Ala	GGG Gly	GAA Glu	Cys	ATC	TAC Tyr	GTC Val	1280	
GAG C	TO (GAG (Glu / 375	GAC (CGC . Arg :	AAG (ela 1	GTC Val 380	TTC Phe	TGG '	TAC .	Asn :	AAG Lys 385	AA G '	TTC Phe	TAGCCGC	CGC 13	335
CGCTC	GCA	GA G	CTGA	GAC	G CT	ACCGI	'AGG	AAT	GGGA	GCA (GAAA	CCAG	GA GO	GAGG	AGACG	1395	
GTACT	'CGC	cc ci	AAAG1	CTC	C GT	CAACO	TAT	CTA	ATCG:	TTA (GTCG:	rcag:	rc T	TTA	GACGG	1455	
GAAGA	GAG	AT C	ATTTC	GGC	A CAC	GAGAC	GAA	GGC'	TTAC	rgc i	AGTG	CCAT	cg ca	raga	GCTGC	1515	

CATCAAGTAC	AAGTAGGCAA	ATTCGTCAAC	TTAGTGTGTC	CCATGTTGTT	TTTCTTAGTC	1575
GTCCGCTGCT	GTAGGCTTTC	CGGCGGCGGT	CGTTTGTGTG	GTTGGCATCC	GTGGCCATGC	1635
CTGTGCGTGC	GTGGCCGCGC	TTGTCGTGTG	CGTCTGTCGT	CGCGTTGGCG	TCGTCTCTTC	1695
GTGCTCCCCG	TGTGTTGTTG	TAAAACAAGA	AGATGTTTTC	TGGTGTCTTT	GGCGGAATAA	1755
CAGATCGTCC	GAACGAAAAA	ааааааааа	AAAAA			1790
(2)	INFORMATIO	ON FOR SEQ	ID NO:8:			

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Ala Gly Gly Arg Met Thr Glu Lys Glu Arg Glu Lys Gln Glu 1 5 10 15

Gln Leu Ala Arg Ala Thr Gly Gly Ala Ala Met Gln Arg Ser Pro Val 20 25 30

Glu Lys Pro Pro Phe Thr Leu Gly Gln Ile Lys Lys Ala Ile Pro Pro 35 40 45

His Cys Phe Glu Arg Ser Val Leu Lys Ser Phe Ser Tyr Val Val His 50 55 60

Asp Leu Val Ile Ala Ala Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile 65 70 75 80

Pro Ala Leu Pro Ser Pro Leu Arg Tyr Ala Ala Trp Pro Leu Tyr Trp 85 90 95

Ile Ala Gln Gly Cys Val Cys Thr Gly Val Trp Val Ile Ala His Glu 100 105 110

Cys Gly His His Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp Val Val 115 120 125

Gly Leu Val Leu His Ser Ser Leu Met Val Pro Tyr Phe Ser Trp Lys 130 135 140

Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp 145 150 155 160

Glu Val Phe Val Pro Lys Lys Glu Ala Leu Pro Trp Tyr Thr Pro 165 170 175

Tyr Val Tyr Asn Asn Pro Val Gly Arg Val Val His Ile Val Val Gln 180 185 190

Leu Thr Leu Gly Trp Pro Leu Tyr Leu Ala Thr Asn Ala Ser Gly Arg 195 200 205

Pro Tyr Pro Arg Phe Ala Cys His Phe Asp Pro Tyr Gly Pro Ile Tyr 210 215 220

Asn Asp Arg Glu Arg Ala Gln Ile Phe Val Ser Asp Ala Gly Val Val 225 230 235 240

Ala Val Ala Phe Gly Leu Tyr Lys Leu Ala Ala Phe Gly Val Trp 245 250 255

Trp Val Val Arg Val Tyr Ala Val Pro Leu Leu Ile Val Asn Ala Trp 260 265 270

Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His 275 280 285

Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Met 290 295 300

Asp Arg Asp Tyr Gly Ile Leu Asn Arg Val Phe His Asn Ile Thr Asp 305 310 315 320

Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala 325 330 335

Met Glu Ala Thr Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His 340 345 350

Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu 355 360 365

Cys Ile Tyr Val Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn 370 380

Lys Lys Phe 385

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 673 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Ricinus communis

	(vii)	IMMEDIA (B) CI		RCE: pRF2-10	:			
	(ix)		E: ME/KEY CATION		573			
	(xi)	SEQUENC	CE DESC	RIPTION	1: SEQ	ID NO:9	:	
TGG GTG ATC Trp Val Met 1	G GCG CAT t Ala His 5	Asp Cys	GGG CA Gly Hi	C CAT GC s His Al 10	C TTC AGT a Phe Ser	GAC TATE Asp Tyr	Gln	48
TTG CTT GAT Leu Leu Asp	F GAT GTA D Asp Val 20	GTT GGT Val Gly	CTT ATC Leu Ile 2	e Leu Hi	C TCC TGT s Ser Cys	CTC CTT Leu Leu 30	GTC Val	96
CCT TAT TTT Pro Tyr Phe 35	e Ser Trp	AAA CAC Lys His	AGC CAS Ser His 40	r CGC CG. B Arg Arg	A CAT CAT g His His 45	TCC AAC Ser Asn	ACA Thr	144
GGG TCC CTG Gly Ser Leu 50	GAA CGG	GAT GAA Asp Glu 55	GTG TTT	GTT CCC	C AAG AAG o Lys Lys 60	AAA TCT Lys Ser	AGT Ser	192
ATC CGT TGG Ile Arg Trp 65	TAT TCC Tyr Ser	AAA TAC Lys Tyr 70	CTC AAC Leu Asr	AAC CC Aan Pro 75	o Pro Gly	CGT ATC Arg Ile	ATG Met 80	240
ACA ATT GCC Thr Ile Ala	GTC ACA Val Thr 85	CTT TCA Leu Ser	CTT GGC Leu Gly	TGG CCT Trp Pro	T CTG TAC D Leu Tyr	CTA GCA Leu Ala 95	TTC . Phe	288
AAT GTT TCA Asn Val Ser	GGC AGG Gly Arg 100	CCA TAT Pro Tyr	GAT CGG Asp Arg 105	Phe Ala	C TGC CAC	TAT GAC Tyr Asp 110	CCA Pro	336
TAT GGC CCG Tyr Gly Pro 115	Ile Tyr	AAT GAT Asn Asp	CGC GAG Arg Glu 120	CGA ATO	GAG ATA Glu Ile 125	TTC ATA Phe Ile	TCA Ser	384
GAT GCT GGT Asp Ala Gly 130	GTT CTT Val Leu	GCT GTC Ala Val 135	ACT TTT Thr Phe	GGT CTC Gly Leu	TAC CAA Tyr Gln 140	CTT GCT Leu Ala	ATA Ile	432
GCG AAG GGG Ala Lys Gly 145	CTT GCT Leu Ala	TGG GTT Trp Val 150	GTC TGT Val Cys	GTA TAT Val Tyr 155	Gly Val	CCA TTG Pro Leu	TTG Leu 160	480
GTG GTG AAT Val Val Asn	TCA TTC Ser Phe 165	CTT GTT Leu Val	CTG ATC Leu Ile	ACA TTT Thr Phe 170	CTG CAG Leu Gln	CAT ACT His Thr 175	CAC 5	528
CCT GCA TTG Pro Ala Leu	CCA CAT Pro His 180	TAT GAT Tyr Asp	TCG TCG Ser Ser 185	GAG TGG Glu Trp	GAC TGG Asp Trp	CTA AGA Leu Arg 190	GGA 5	576

GCT Ala	CTA Leu	GCA Ala 195	ACT Thr	GTT Val	GAC Asp	AGA Arg	GAT Asp 200	TAC Tyr	GGG Gly	ATC Ile	TTG Leu	AAC Asn 205	AAG Lys	GTG Val	TTC Phe	
CAT His	AAC Asn 210	ATA Ile	ACG Thr	GAC Asp	ACT Thr	CAA Gln 215	GTA Val	GCT Ala	CAC His	CAC His	CTT Leu 220	TTC Phe	ACC Thr	ATG Met	CCC Pro	С
	(2)	I	NFO	RMAI	CION	FO	R SE	EQ I	D N	0:10	:					
			(i)	SEQ (A (B (D) I	LENG TYPE		22 amir	24 a 10 a	min		cids				
		(ii)	MOL	ECU	LE :	TYPE	:	pro	ceir	1					
		(xi)	SEÇ	UEN	CE I	DESC	RIP	TIOI	V :	SEQ	ID	NO:	10:		
	Trp 1	Val	Met	Ala	His 5	Asp	Cys	Gly	His	His 10	Ala	Phe	Ser	Asp	Tyr 15	Gln
	Leu	Leu	Asp	Asp 20	Val	Val	Gly	Leu	Ile 25	Leu	His	Ser	Cys	Leu 30	Leu	Val
	Pro	Tyr	Phe 35	Ser	Trp	Lys	His	Ser	His	Arg	Arg	His	His 45	Ser	Asn	Thr
	Gly	Ser 50	Leu	Glu	Arg	Asp	Glu 55	Val	Phe	Val	Pro	Lys 60	Lys	Lys	Ser	Seı
	Ile 65	Arg	Trp	Tyr	Ser	Lys 70	Tyr	Leu	Asn	Asn	Pro 75	Pro	Gly	Arg	Ile	Met 80
	Thr	Ile	Ala	Val	Thr 85	Leu	Ser	Leu	Gly	Trp 90	Pro	Leu	Tyr	Leu	Ala 95	Phe
	Asn	Val	Ser	Gly 100	Arg	Pro	Tyr	Asp	Arg 105	Phe	Ala	Cys	His	Tyr 110	Asp	Pro
	Tyr	Gly	Pro 115	Ile	Tyr	Asn	Asp	Arg 120	Glu	Arg	Ile	Glu	Ile 125	Phe	Ile	Ser
	Asp	Ala 130	Gly	Val	Leu	Ala	Val 135	Thr	Phe	Gly	Leu	Tyr 140	Gln	Leu	Ala	Ile
	Ala 145	Lys	Gly	Leu	Ala	Trp 150	Val	Val	Cys	Val	Tyr 155	Gly	Val	Pro	Leu	Leu 160
	Val	Val	Asn	Ser	Phe 165	Leu	Val	Leu	Ile	Thr 170	Phe	Leu	Gln	His	Thr 175	His
	Pro	Ala	Leu	Pro 180	His	Tyr	Asp	Ser	Ser	Glu	Trp	Asp	Trp	Leu 190	Arg	Gly

Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe
195 200 205

His Asn Ile 1 210	hr Asp Thr Gln Va 215	l Ala His His Leu 220	Phe Thr Met Pro
(2) INFORM	ATION FOR SEQ 1	ID NO:11:	
(i)	(B) TYPE: nu	1369 base pairs cleic acid ESS: double	
(ii)	MOLECULE TYPE:	cDNA	
(iii)	HYPOTHETICAL:	NO	
(iv)	ANTI-SENSE: N	0	
(vi)	ORIGINAL SOURC	E: Ricinus commur	nis
(vii)	IMMEDIATE SOUR (B) CLONE: pr		
(ix)	FEATURE: (A) NAME/KEY: (B) LOCATION:	CDS 1841347	
(xi)	SEQUENCE DESCR	IPTION: SEQ ID	NO:11:
CGGCCGGGAT TCCGGTTT	TC ACACTAATTT GCA	AAAAATG CATGATTTCA	A CCTCAAATCA 60
AACACCACAC CTTATAAC	TT AGTCTTAAGA GAG	AGAGAGA GAGGAGACAT	TTCTCTTCTC 120
TGAGATGAGC ACTTCTCT			
AGA ATG GGA GGT GGT Met Gly Gly Gly 1	GGT CGC ATG TCT Gly Arg Met Ser 5	ACT GTC ATA ATC AG Thr Val Ile Ile Se 10	C AAC AAC 228 r Asn Asn 15
AGT GAG AAG AAA GGA Ser Glu Lys Lys Gly 20	GGA AGC AGC CAC Gly Ser Ser His	CTG GAG CGA GCG CC Leu Glu Arg Ala Pr 25	G CAC ACG 276 o His Thr 30
AAG CCT CCT TAC ACA Lys Pro Pro Tyr Thr 35	CTT GGT AAC CTC Leu Gly Asn Leu 40	Lys Arg Ala Ile Pr	A CCC CAT 324 o Pro His 5
IGC TTT GAA CGC TCT Cys Phe Glu Arg Ser 50	TTT GTG CGC TCA Phe Val Arg Ser	TTC TCC AAT TTT GC Phe Ser Asn Phe Al 60	C TAT AAT 372 a Tyr Asn
TTC TGC TTA AGT TTT The Cys Leu Ser Phe 65	CTT TCC TAC TCG I Leu Ser Tyr Ser I 70	ATC GCC ACC AAC TTG Ile Ala Thr Asn Pho	C TTC CCT 420 e Phe Pro

TAC Tyr 80	ATC Ile	TCT Ser	TCT Ser	CCG Pro	CTC Leu 85	Ser	TAT Tyr	GTC Val	GCT Ala	TGG Trp 90	Leu	GTT Val	TAC Tyr	TGG Trp	CTC Leu 95	468
													CAT			516
GGC Gly	CAT	CAT His	GCT Ala 115	TTT Phe	AGT Ser	GAG Glu	TAT Tyr	CAG Gln 120	CTG Leu	GCT Ala	GAT Asp	GAC Asp	ATT Ile 125	GTT Val	GGC Gly	564
CTA Leu	ATT Ile	GTC Val 130	CAT His	TCT Ser	GCA Ala	CTT Leu	CTG Leu 135	GTT Val	CCA Pro	TAT Tyr	TTT Phe	TCA Ser 140	TGG Trp	AAA Lys	TAT Tyr	612
AGC Ser	CAT His 145	CGC Arg	CGC Arg	CAC His	CAT His	TCT Ser 150	AAC Asn	ATA Ile	GGA Gly	TCT Ser	CTC Leu 155	GAG Glu	CGA Arg	GAC Asp	GAA Glu	660
GTG Val 160	TTC Phe	GTC Val	CCG Pro	AAA Lys	TCA Ser 165	AAG Lys	TCG Ser	AAA Lys	ATT Ile	TCA Ser 170	TGG Trp	TAT Tyr	TCT Ser	AAG Lys	TAC Tyr 175	708
													ACG Thr			756
													AGA Arg 205			804
GAT Asp	CGC Arg	TTT Phe 210	GCT Ala	TGC Cys	CAT His	TAT Tyr	GAT Asp 215	CCC Pro	TAT Tyr	GGC Gly	CCA Pro	ATA Ile 220	TTT Phe	TCC Ser	GAA Glu	852
													TTT Phe			900
ACG Thr 240	TTT Phe	GTG Val	CTT Leu	TAT Tyr	CAG Gln 245	GCT Ala	ACA Thr	ATG Met	GCA Ala	AAA Lys 250	GGG Gly	TTG Leu	GCT Ala	TGG Trp	GTA Val 255	948
ATG Met	CGT Arg	ATC Ile	TAT Tyr	GGG Gly 260	GTG Val	CCA Pro	TTG Leu	CTT Leu	ATT Ile 265	GTT Val	AAC Asn	TGT Cys	TTC Phe	CTT Leu 270	GTT Val	996
ATG Met	ATC Ile	ACA Thr	TAC Tyr 275	TTG Leu	CAG Gln	CAC His	ACT Thr	CAC His 280	CCA Pro	GCT Ala	ATT Ile	CCA Pro	0GC Arg 285	TAT Tyr	330 Gly	1044
													GTC Val			1092

GAT Asp	TAT Tyr 305	GGG Gly	GTG Val	TTG Leu	AAT Asn	AAA Lys 310	GTA Val	TTC Phe	CAT His	AAC Asn	ATT Ile 315	GCA Ala	GAC Asp	ACT Thr	CAT His		1140
GTA Val 320	GCT Ala	CAT His	CAT His	CTC Leu	TTT Phe 325	GCT Ala	ACA Thr	GTG Val	CCA Pro	CAT His 330	TAC Tyr	CAT His	GCA Ala	ATG Met	GAG Glu 335		1188
GCC Ala	ACT Thr	AAA Lys	GCA Ala	ATC Ile 340	AAG Lys	CCT Pro	ATA Ile	ATG Met	GGT Gly 345	GAG Glu	TAT Tyr	TAC Tyr	CGG Arg	TAT Tyr 350	GAT Asp		1236
GGT Gly	ACC Thr	CCA Pro	TTT Phe 355	TAC Tyr	AAG Lys	GCA Ala	TTG Leu	TGG Trp 360	AGG Arg	GAG Glu	GCA Ala	AAG Lys	GAG Glu 365	TGC Cys	TTG Leu		1284
TTC Phe	GTC Val	GAG Glu 370	CCA Pro	GAT Asp	GAA Glu	GGA Gly	GCT Ala 375	CCT Pro	ACA Thr	CAA Gln	GGC Gly	GTT Val 380	TTC Phe	TGG Trp	TAC Tyr		1332
	AAC Asn 385			TAAA	AAAG	TG T	CATO	TAGO	C TG	CCG							1369
	(2)	I	NFOI	RMAT	ION	FOR	SE	QII	ON C	:12:	:						
			(i)	SEQ (A) (B) (D)	L T	ENGT YPE:	ГН: : а	ACTE 38 mind	7 am	ino id		.ds					
		(ii)	MOL	ECU	LE I	YPE	: p	rot	ein							
		(xi)	SEQ	UEN	CE D	ESC	RIPI	CION	_		י חד	vi∩ • 1	2:			
	Met 1	Gly	Gly	Gly	Gly	Ara	Mot			: :	SEQ.	10 1	.,0.1				
					5	9	met	Ser	Thr						Asn 15	Ser	
	Glu	Lys	Lys		5					Val 10	Ile	Ile	Ser	Asn	15		
		Lys Pro		Gly 20	5 Gly	Ser	Ser	His	Leu 25	Val 10 Glu	Ile Arg	Ile Ala	Ser Pro	Asn His 30	15 Thr	Lys	
	Pro		Tyr 35	Gly 20 Thr	5 Gly Leu	Ser	Ser	His Leu 40	Leu 25 Lys	Val 10 Glu Arg	Ile Arg Ala	Ile Ala Ile	Ser Pro Pro 45	Asn His 30 Pro	15 Thr His	Lys Cys	
	Pro Phe	Pro Glu	Tyr 35 Arg	Gly 20 Thr	5 Gly Leu Phe	Ser Gly Val	Ser Asn Arg 55	His Leu 40 Ser	Leu 25 Lys Phe	Val 10 Glu Arg Ser	Ile Arg Ala Asn	Ile Ala Ile Phe 60	Ser Pro Pro 45 Ala	Asn His 30 Pro	15 Thr His	Lys Cys Phe	
	Pro Phe Cys 65	Pro Glu 50	Tyr 35 Arg	Gly 20 Thr Ser	5 Gly Leu Phe	Ser Gly Val Ser	Ser Asn Arg 55	His Leu 40 Ser	Leu 25 Lys Phe	Val 10 Glu Arg Ser	Ile Arg Ala Asn Thr 75	Ile Ala Ile Phe 60 Asn	Pro Pro 45 Ala	Asn His 30 Pro Tyr	15 Thr His Asn	Lys Cys Phe Tyr 60	

His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu 120 Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val 150 Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp 200 Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala 325 330 Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly 345 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg Asn Lys Tyr

(2)	INFOR	MATION FOR SEQ ID NO:13:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: CDNA	
	(iii)	HYPOTHETICAL: NO	
	(iv)	ANTI-SENSE: NO	
	(ix)	FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 123 (D) OTHER INFORMATION: /product= "synthetic oligonucleotide"	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:13:	
TGGGT	TATGCC	AYGANTGYGG NCA	23
(2)	INFORM	MATION FOR SEQ ID NO:14:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) TRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(iii)	HYPOTHETICAL: NO	
	(iv)	ANTI-SENSE: NO	
	(ix)	FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 122 (D) CTHER INFORMATION: /product=	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:14:	
AAART	GRTGG C	CACRTGNGTR TC	22

(2)	INFORMAT	ION FOR SEQ ID NO:15:
	(<i>I</i> (E (C	EQUENCE CHARACTERISTICS: A) LENGTH: 2973 base pairs B) TYPE: nucleic acid C) STRANDEDNESS: double D) TOPOLOGY: linear
	(ii) MO	DLECULE TYPE: DNA (genomic)
	(iii) HY	YPOTHETICAL: NO
	(iv) AN	VTI-SENSE: NO
		RIGINAL SOURCE: A) ORGANISM: Arabidopsis thaliana
		MEDIATE SOURCE: 3) CLONE: pAGF2-6
		CATURE: NAME/KEY: exon LOCATION: 433520
		ATURE:) NAME/KEY: intron) LOCATION: 5211654
	(xi) SE	QUENCE DESCRIPTION: SEQ ID NO:15:
ATTCGGTAAT	TCCTACATAT	TTTAGAGATT AGTTTGAGTT TCCATCCATA CTTTACTAGT 60
GATTATAAAT	TTAAAATACG	TACTTTTCGA CTATAAAGTG AAACTAAGTA AATTAGAACG 120
TGATATTAAA	AAGTTAATGT	TCACTGTTAT ATTTTTTCA CAAGTAAAAA ATGGGTTATT 180
TGCGGTAAAT	AAAAATACCA	GATATTTTGA ATTGATTAAA AAGGTTGAAA TAAGAGAGGA 240
GGGGAAAGAA	AAGAAGGTGG	GGGCCCAGTA TGAAAGGGAA AGGTGTCATC AAATCATCTC 300
TCTCTCTCTC	TACCTTCGAC	CCACGGGCCG TGTCCATTTA AAGCCCTGTC TCTTGCCATT 360
CCCCATCTGA	CCACCAGAAG	AAGAGCCACA CACTCACAAA TTAAAAAGAG AGAGAGAGAG 420
AGAGAGACAG	AGAGAGAGAG	AGATTCTGCG GAGGAGCTTC TTCTTCGTAG GGTGTTCATC 480
STTATTAACG	TTATCGCCCC	TACGTCAGCT CCATCTCCAG GTCCGTCGCT TCTCTTCCAT 540

TTCTTCTCAT TTTCGATTTT GATTCTTATT TCTTTCCAGT AGCTCCTGCT CTGTGAATTT

CTCCGCTCAC GATAGATCTG CTTATACTCC TTACATTCAA CCTTAGATCT GGTCTCGATT

CTCTGTTTCT CTGTTTTTT CTTTTGGTCG AGAATCTGAT GTTTGTTTAT GTTCTGTCAC

CATTAATAAT GATGAACTCT CTCATTCATA CAATGATTAG TTTCTCTCGT CTACCAAACG

600

660

720

ATATGTTGC.	A TTTTCACTT	r TCTTCTTTT	TTCTAAGATO	ATTTGCTTT(G ACCAATTTGT	840
TTAGATCTT	r attttattti	T ATTTTCTGGT	GGGTTGGTGG	AAATTGAAA	AAAAAAAAA	900
AAAAGCATAA	A ATTGTTATTI	GTTAATGTAT	TCATTTTTTG	GCTATTTGTT	CTGGGTAAAA	960
ATCTGCTTCT	r actgttgaat	CTTTCCTGGA	TTTTTTACTC	CTATTGGGTT	TTTATAGTAA	1020
AAATACATAA	A TAAAAGGAAA	ACAAAAGTTT	TATAGATTCT	CTTAAACCCC	TTACGATAAA	1080
AGTTGGAATC	C AAAATAATTC	AGGATCAGAT	GCTCTTTGAT	TGATTCAGAT	GCGATTACAG	1140
TTGCATGGAA	AATTTTCTAG	ATCCGTCGTC	ACATTTTATT	TTCTGTTTAA	ATATCTAAAT	1200
CTGATATATG	ATGTCGACAA	ATTCTGGTGG	CTTATACATC	ACTTCAACTG	TTTTCTTTTG	1260
GCTTTGTTTG	TCAACTTGGT	TTTCAATACG	ATTTGTGATT	TCGATCGCTG	AATTTTTAAT	1320
ACAAGCAAAC	TGATGTTAAC	CACAAGCAAG	AGATGTGACC	TGCCTTATTA	ACATCGTATT	1380
ACTTACTACT	AGTCGTATTC	TCAACGCAAT	CGTTTTTGTA	TTTCTCACAT	TATGCCGCTT	1440
CTCTACTCTT	TATTCCTTTT	GGTCCACGCA	TTTTCTATTT	GTGGCAATCC	CTTTCACAAC	1500
CTGATTTCCC	ACTTTGGATC	ATTTGTCTGA	AGACTCTCTT	GAATCGTTAC	CACTTGTTTC	1560
TTGTGCATGC	TCTGTTTTT	AGAATTAATG	ATAAAACTAT	TCCATAGTCT	TGAGTTTTCA	1620
GCTTGTTGAT	TCTTTTGCTT	TTGGTTTTCT	GCAGAAACAT	GGGTGCAGGT	GGAAGAATGC	1680
CGGTTCCTAC	TTCTTCCAAG	AAATCGGAAA	CCGACACCAC	AAAGCGTGTG	CCGTGCGAGA	1740
AACCGCCTTT	CTCGGTGGGA	GATCTGAAGA	AAGCAATCCC	GCCGCATTGT	TTCAAACGCT	1800
CAATCCCTCG	CTCTTTCTCC	TACCTTATCA	GTGACATCAT	TATAGCCTCA	TGCTTCTACT	1860
ACGTCGCCAC	CAATTACTTC	TCTCTCCTCC	CTCAGCCTCT	CTCTTACTTG	GCTTGGCCAC	1920
TCTATTGGGC	CTGTCAAGGC	TGTGTCCTAA	CTGGTATCTG	GGTCATAGCC	CACGAATGCG	1980
GTCACCACGC	ATTCAGCGAC	TACCAATGGC	TGGATGACAC	AGTTGGTCTT	ATCTTCCATT	2040
CCTTCCTCCT	CGTCCCTTAC	TTCTCCTGGA	AGTATAGTCA	TCGCCGTCAC	CATTCCAACA	2100
CTGGATCCCT	CGAAAGAGAT	GAAGTATTTG	TCCCAAAGCA	GAAATCAGCA	ATCAAGTGGT	2160
ACGGGAAATA	CCTCAACAAC	CCTCTTGGAC	GCATCATGAT	GTTAACCGTC	CAGTTTGTCC	2220
TCGGGTGGCC	CTTGTACTTA	GCCTTTAACG	TCTCTGGCAG	ACCGTATGAC	GGGTTCGCTT	2230
GCCATTTCTT	CCCCAACGCT	CCCATCTACA .	ATGACCGAGA	ACGCCTCCAG	ATATACCTCT	2340
CTGATGCGGG	-TATTCTAGCC	GTCTGTTTTG (GTCTTTACCG	TTACGCTGCT	GCACAAGGGA	2400
TGGCCTCGAT	GATCTGCCTC	TACGGAGTAC (CGCTTCTGAT	AGTGAATGCG	TTCCTCGTCT	2460
TGATCACTTA	CTTGCAGCAC	ACTCATCCCT (CGTTGCCTCA	CTACGATTCA	TCAGAGTGGG	2520

ACTGGCTCAG	GGGAGC	TTTG G	CTACCGTAG	ACAGAGACTA	CGGAATCTTG	AACAAGGTGT	2580
TCCACAACAT	TACAGA	CACA C	ACGTGGCTC	ATCACCTGTT	CTCGACAATG	CCGCATTATA	2640
ACGCAATGGA	AGCTAC	AAAG G	CGATAAAGC	CAATTCTGGG	AGACTATTAC	CAGTTCGATG	2700
GAACACCGTG	GTATGT	GGCG A	TGTATAGGG	AGGCAAAGGA	GTGTATCTAT	GTAGAACCGG	2760
ACAGGGAAGG	TGACAA	GAAA G	GTGTGTACT	GGTACAACAA	TAAGTTATGA	GGATGATGGT	2820
GAAGAAATTG	TCGACT	TTTC T	CTTGTCTGT	TTGTCTTTTG	TTAAAGAAGC	TATGCTTCGT	2880
TTTAATAATC	TTATTG	CCA T	TTTGTTGTG	TTATGACATT	TTGGCTGCTC	ATTATGTTAT	2940
GTGGGAAGTT	AGCGTTC	CAAA TO	GTTTTGGGT	CGG			2973
(2)	INFORM	ATION	FOR SEQ	ID NO:16	!		
	(i)	(A) (B) (C)	LENGTH: TYPE: STRANDE	RACTERIST: 23 base nucleic ac DNESS: si Y: linear	pairs cid ingle		
	(ii)	MOLE	CULE TYP	E: cDNA			
	(iii)	НҮРО	THETICAL	: NO			
	(iv)	ANTI	-sense:	NO			
	(ix)	(B)	NAME/KE LOCATION	Y: misc_f N: 123 NFORMATION	: /produ "synth		
	(xi)	SEQU	ENCE DES	CRIPTION:	SEQ ID N	0:16:	
GGGCA'	IGTNG A	RAANA	ARRTG RTO	3			23
(2)	INFORMA	ATION	FOR SEQ	ID NO:17:			
	(i)	(A)	LENGTH: TYPE: r STRANDER	RACTERISTI 23 base nucleic ac DNESS: si Y: linear	pairs id ngle		
	· (ii)	MOLE	CULE TYPI	E: cDNA			

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature (B) LOCATION: 1..23

(D) OTHER INFORMATION: /product= "synthetic

oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGCATGTRC TRAANARRTG RTG

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: JONATHAN EDWARD LIGHTNER JOHN JOSEPH OKULEY
 - (ii) TITLE OF INVENTION: GENES FOR MICROSOMAL FATTY ACID DELTA-12 DESATURASES AND RELATED ENZYMES FROM PLANTS
 - (iii) NUMBER OF SEQUENCES: 17
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
 - (B) STREET: 1007 MARKET STREET
 - (C) CITY: WILMINGTON
 - (D) STATE: DELAWARE
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 19898
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk

 - (B) COMPUTEE: MacIntosh(C) OPERATING SYSTEM: Microsoft Windows 95
 - (D) SOFTWARE: Microsoft Word Version 7.0
 - (vi) CURPENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (vii) PRIOF APPLICATION DATA:
 - (A) APPLICATION NUMBER: U.S. 07/977,339
 - FILING DATE: 17-NOV-1992 (B)
 - (A) APPLICATION NUMBER: U.S. 09/133,962
 - (B) FILING DATE: 14-AUG-1998
 - (viii) ATTOPNEY/AGENT INFORMATION:
 - (A) NAME: Christenbury, Lynne M..
 - (B) PEGISTRATION NUMBER: 30,971
 - (C) FEFEFENCE/DOCKET NUMBER: BB1043 US DIV
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (302) 992-5481
 - TELEFAX: (301) 892-1026
 - TFLEM: 835470 (C)
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1372 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Arabidopsis thaliana
- (vii) IMMEDIATE SOURCE:
- (B) CLONE: p92103
- (ix) FEATURE:
- (A) NAME/KEY: CDS
- (B) LOCATION: 93..1244
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGAGAGAGA ATTOTGOGGA GGAGOTTOTT OTTOGTAGGG TGTTCATCGT TATTAACGTT

ATCGCCCCTA CGTCAGCTCC ATCTCCAGAA AC ATG GGT GCA GGT GGA AGA ATG

Met Gly Ala Gly Gly Arg Met

CCG GTT CCT ACT TCT TCC AAG AAA TCG GAA ACC GAC ACA AAG CGT $1\,6\,1$

Pro Val Pro Thr Ser Ser Lys Lys Ser Glu Thr Asp Thr Thr Lys Arg

GTG CCG TGC GAG AAA CCG CCT TTC TCG GTG GGA GAT CTG AAG AAA GCA 209

Val Pro Cys Glu Lys Pro Pro Phe Ser Val Gly Asp Leu Lys Lys Ala 25 - 30 - 35

ATC CCG CCG CAT TGT TTC AAA CGC TCA ATC CCT CGC TCT TTC TCC TAC 257

ile Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr 40 45 50 55

CTI ATO AGI GAG ATO ATI ATA GOU TOA IGO TIO IAC TAO GIO GOU ACC -305

Let lie Son Asplice Let Le Arade. Sys Fle Pyr Tyr wi Ara Thr 60 65 70

AAT TAC TTO TOT CTC CTC CCT CAG CCT CTC TCT TAC TTG GCT TGG CCA 353

Ash Tyr Phe Ser Leu Eeu Pro Glin Pro Leu Ser Tyr Leu Ala Trp Pro 75 80 85

CTC TAT TGG GCC TGT CAA GGC TGT GTC CTA ACT GGT ATC TGG GTC ATA $\pm 4/4$

Leu Tyr Trp Ala Cys Gln Gly Cys Val Leu Thr Gly Ile Trp Val Ile 95 90 10û GOO CAC GAA TGO GGT CAC CAC GOA TTO AGO GAC TAC CAA TGG CTG GAT Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Tro Leu Asp 105 GAC ACA GTT GGT CTT ATC TTC CAT TCC TTC CTC CTC GTC CCT TAC TTC Asp Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe 125 130 TOO TGG AAG TAT AGT CAT CGO CGT CAC CAT TOO AAC ACT GGA TOO CTC Ser Trp Lys Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu 140145 GAA AGA GAT GAA GTA TTT GTC CCA AAG CAG AAA TCA GCA ATC AAG TGG 593 Glu Arg Asp Glu Val Phe Val Pro Lys Gln Lys Ser Ala Ile Lys Trp 155 160 TAC GGG AAA TAC CTC AAC AAC CCT CTT GGA CGC ATC ATG ATG TTA ACC -6.41Tyr Gly Lys Tyr Leu Asn Asn Pro Leu Gly Ard Ile Met Met Leu Thr 170 GTC CAG TTT GTC CTC GGG TGG CCC TTG TAC TTA GCC TTT AAC GTC TCT Val Glm Phe Val Leu Gly Trp Pro Leu Tyr Leu Ala Phe Ash Val Ser GGC AGA COG TAT GAC GGG TTC GGT TGC CAT TTC TTC CCC AAC GGT CCC Gly Ard Pro Tyr Asp Gly Phe Ala Cys His Phe Phe Pro Ash Ala Pro 205 210 215 ATC TAC AAT GAC CGA GAA CGC CTC CAG ATA TAC CTC TCT GAT GCG GGT 725 Ile Tyr Ash Asp Arq Glu Ard Leu Gln Ile Tyr Leu Ser Asp Ala Gly 225 220 ATT CTA GCC GTC TGT TTT GGT CTT TAC CGT TAC GCT GCT GCA CAA GGG The Lew Ala Val Cys Phe Gly Lod Tyr Ara Tyr Ala Ala Ala Gin Gly APS 300 TES ATS ATS TES CTS TAC 35A 3TA SOS CTT CTS ATA GTS AAT 991 Met Ala Ser Met Ile Cys Leu Tyr Gly Val Pro Leu Leu Ile Val Asn ည်းနှင့် 2 E. C. 260 GOG TTO OTO GTO TTG ATO ACT TAC TTG CAG CAC ACT CAT CCC TCG TTG Ala Phe Leu Val Leu Ile Thr Tyr Le. Gin His Thr His Pro Ser Leu 265 270 275

CCT CAC TAC GAT TCA TCA GAG TGG GAC TGG CTC AGG GGA GCT TTG GCT 977

Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala 280 285 290 290

ACC GTA GAC AGA GAC TAC GGA ATC TTG AAC AAG GTG TTC CAC AAC ATT 1025

Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile 300 305 310

ACA GAC ACA CAC GTG GCT CAT CAC CTG TTC TCG ACA ATG CCG CAT TAT 1073

Thr Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr 315 320 325

AAC GCA ATG GAA GCT ACA AAG GCG ATA AAG CCA ATT CTG GGA GAC TAT 1121

Asn Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile Leu Gly Asp Tyr 330 335 340

TAC CAG TTC GAT GGA ACA CCG TGG TAT GTA GCG ATG TAT AGG GAG GCA 1169

Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu Ala 345 - 350 - 355

AAG GAG TGT ATC TAT GTA GAA COG GAC AGG GAA GGT GAC AAG AAA GGT 1217

Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly Asp Lys Lys Gly 360 370 375

GTG TAC TGG TAC AAC AAT AAG TTA TGAGCATGAT GGTGAAGAAA TTGTCGACCT

Val Tyr Trp Tyr Asn Asn Lys Leu 380

TTCTCTTGTC TGTTTGTCTT TTGTTAAAGA AGCTATGCTT CGTTTTAATA ATCTTATTGT

CCATTTGTT GTGTTATGAC ATTTTGGCTG CTCATTATGT T 1372

- (1) INFORMATION FOR SEQ 10 NO:2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) belvoik: bés amins acias
 - (B) TYPE: amino acid
 - (U) idromout inear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser

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Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser Cys Phe Tyr Tyr Val Ala Thr Ash Tyr Phe Ser Leu Leu Pro Gln Pro Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gin Gly Cys Val Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 105 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His 135 His Ser Asn Thr Gly Ser Leu Glu Ard Asp Glu Val Phe Val Pro Lys Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 165 Gly Ard Ile Met Met Leu Thr Val Glr. Phe Val Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys 200 195 His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln 215 Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr Ard Tyr Ala Ala Ala Clo Cly Met Ala Ser Met Ile Cvs Leu Tyr Glv Val Pro Let Den 71e Var Ash Ala Pho Let val Let 11e Inr lyr Let 200 Gla His Thr His Pro Ser Let Pro His Tyr Asp Ser Ser Glu Tro Asp 280 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Ash Lys Val Phe His Ash Ile Thr Asp Thr His Val Ala His His Lou

305					310					315					320	
Phe	Ser	Thr	Met	Pro 325	His	Tyr	Asn	Ala	Met 330	Glu	Ala	Thr	Lys	Ala 335	Ile	
Lys	Pro	Ile	Leu 340	Gly	Asp	Tyr	Tyr	Gln 345	Phe	Asp	Gly	Thr	Pro 350	Trp	Tyr	
Val	Ala	Met 355	Tyr	Arg	Glu	Ala	Lys 360	Glu	Суѕ	Ile	Tyr	Val 365	Glu	Pro	Asp	
Arg	Glu 370	Gly	Asp	Lys	Lys	Gly 375	Val	Tyr	Trp	Tyr	Asn 330	Asn	Lys	Leu		
(2)		INFO	DRMAT	rion	FOF	SEQ	ID 1	40:3:	:							
		(A) (B) (C)	LENG TYPE STRA TOPG	GTH: E: ru Andei	aclei DNESS	5 bas lc ac S: si	se pa cid ingle	airs	STICS	5:						
		(ii))	MOLI	ECULE	TY:	PE:	cDNA	A to	mP.NA	A					
		7ii:	i)	HYE9	OTHE	ricai	_: 1	40								
) OF:GA						5							
		(A)) NAME LOCA	E/KE		DS	1284									
		(xi))	SEQU	JENCE	E DES	SCRI	PTI 01	1: S	SEQ I	ID NO	0:3:				
GGCA	ACGAC	GCT (CGTG	CCGAA	AT TO	CGGCA	ACGA(G AGO	GAGA(CAGA	GAG	AGAG!	rrr (GAGGA	AGGAGC	50
TTC	rregi	rag (GGTT	CATC	GT TA	ATTA	ACGTI	r aaa	ATCT	CAT	CCC	adadi	rac (GTCAC	GCCAGC	120
TCAA	AGAAA		rg go et gl l								al Je					168
			GAA Glu													216
			GTC Val													264
			ATC Ile													312
ATA	23/7/2	TUC	TGT	TTC	TAC	TAI	GTC	9.77	KCC	ACT	TAC	TTC	CCT	CTC	CTC	160

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Ile	Ala	Ser	Cys 65	Phe	Tyr	Tyr	Val	Ala 70	Thr	Thr	Tyr	Phe	Pro 75	Leu	Leu	
			CTC Leu													408
			CTA Leu													456
			AGC Ser													504
			TTC Phe													552
			CAT His 145													600
			AAG Lys													£48
			GGA Gly													696
			TAC Tyr													744
			TGC Cys													792
			CAG Gln 225			_						_			TGC Cys	840
			TAC Tyr												GTC Val	888
TGC 75			GGA Biy													936
			TTG Leu													98.1
TCT	GAG	TGG	GAT	TGG	TTG	AGG	GGA	G TT	TTG	GCC	ACC	.11. 	GAC	AGA	GAC	1032

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Ser	Glu	Trp	Asp	Trp 290	Leu	Arg	Gly	Ala	Leu 295	Ala	Thr	Val	Asp	Arg 300	Asp	
	GGA Gly															1080
	CAT His															1128
	AAG Lys 335	Ala														1176
	CCG	GTG	GTT	AAG	GCG	ATG	TGG	AGG	GAG	GCG	AAG	GAG	TGT	ATC	TAT	12
24 Thr 350	Pro	Val	Val	Lys	Ala 355	Met	Trp	Arg	Glu	Ala 360	Lys	Glu	Cys	Il⊖	Tyr 365	
GTG 72	GAA	CCG	GAC	AGG	CAA	GGT	GAG	AAG	AAA	GGT	GTG	TTC	TGG	TAC	AAC	12
	Glu	Pro	Asp	Arg 370	Gln	Gly	Glu	Lys	Lys 375	Gly	Val	Phe	Trp	Tyr 380	Asn	
AAT 24	AAG	TTA	TGA	AGC!	AAAGA	AAG A	AAACI	rgaa(CC T	TTCT	CTTC	TA T	GATT (FTCT		1.3
	БуЗ	⊒€ü														
TTG' 84	TTTA	AGA A	AGCTA	ATGT	rr ci	rgtti	rcaar	r AAt	CTTA	AATT	ATC	CATT	rrg 1	rtgro	GTTTT(C 13
TGA(26	CATT	rtg (GCTAA	TAAA	ra To	gTGA:	rgtto	G GA≯	AGTTA	AGTG	TC					14
(2)	INFO	ORMAI	LION	FOF.	SEQ	1 CI	NO:4:	:								
		(i) (A) (B) (D)	LEN	GTH: E: ar	384 nirwo	E CHA amir acid inear	no ac d		STICS	S:						
		(ii))	MOI.E	CHLE	E TYI	PE: p	orote	ein							
		(xi	ì	SEÇ	JEH. E	E DE:	BIRT	-''l' I + il	V: .V	Q II	1 407	:4:				
Met	jlγ	Ala	Gl;	G1 y 5	Arg	Met	Gln	Val	Ser 	Pro	Pro	Ser	Lys	Lys 13	Ser	
Giu	inr	Asp	Ash 20	lle	L∵s	Arg	√aı.	Pro 25	Sys	<i>3</i> lu	rnr	Pro	Pro 30	Phe	Thr	
Val																

RB1043 US CNT1 Seq listing.tx

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 55 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 120 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu Gly Ard Thr Val Met Leu Thr Val Glr. Phe Thr Leu Gly Trp Pro Leu 180 180 Tyr Leu Ala Phe Ash Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala Cys His Phe His Pro Asr. Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr 245 Gly Val Pro Leu Leu Ile Val Asr. Gly Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Let Arg Gly Ala Let Ala Thr Val Asp Arg Asp Tyr Gly Ile Lou Ash Lys lar she his Ash Tie Thr Asp Inr His Fal Ala His His 315 305 310 Len Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala 330 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val

Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro 355 360 365

Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu 370 380

- (2) INFORMATION FOR SEQ ID NO:5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Glycine max
 - (vii) IMMEDIATE SOUPCE:
 - (B) CLONE: pSF2-165F
 - (ix) FEATURE:
 - (A) NAME/HEY: CDS
 - (B) LOCATION: 105..1247
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCATATACTA ATATTTGCTT GTATTGATAG CCCCTCCGTT CCCAAGAGTA TAAAACTGCA

TOGAATAATA CAAGOCACTA GGCATGGGTC TAGCAAAGGA AACAACA ATG GGA GGT 116

Met Gly Gly

AGA GGT CGT GTG GCC AAA GTG GAA GTT CAA GGG AAG AAG CCT CTC TCA

Ard Gly Ard Val Ala 50s Val Glu Val Gln Gly 5ys 5vs Pro Leu Ser 5 10 10

Area GII GUA AAN AMA AMA SOA UNA TIU ANT GIT GGU MA DIT AAN AAN

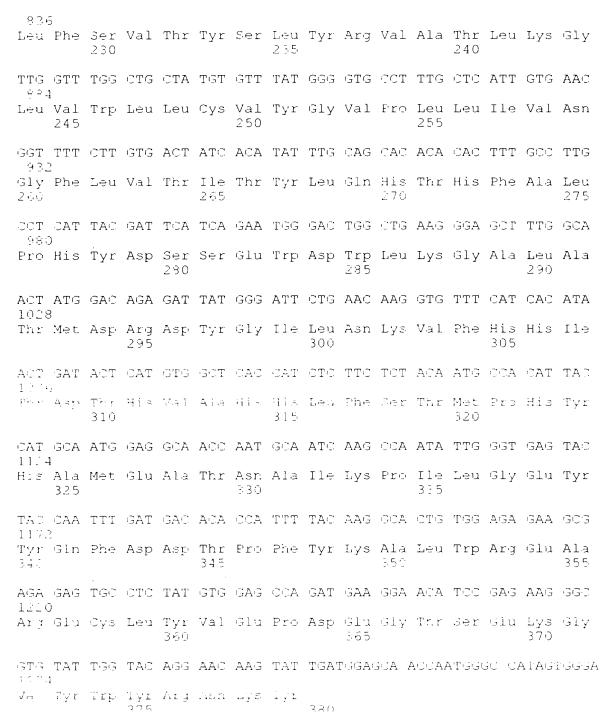
Arg Val Pro Asi. Thi Lys Pro Pro Phe Thi Val Gly Gli Leu Lys Lys 20 35

GIN ATT COM COM CAS THE TIT DAG COS TOO CITC ACT TOA TITC TOO $2\,60$

Ala Ile Pro Pro His Cys Phe Gln Arg Ser Leu Leu Thr Ser Phe Ser 40 45 50

BB1043 US CNT1 Seq listing.t:

TAT GTT GTT TAT GAC CTT TOA TTT GOO TTO ATT TTO TAG ATT GOO ACC 308 Tyr Val Val Tyr Asp Leu Ser Phe Ala Fhe Ile Phe Tyr Ile Ala Thr 5.5 60 AGG TAG TTO CAG OTG OTT OCT CAA OGG TTT TOO OTG ATT GCA TGG OCA Thr Tyr Phe His Leu Leu Pro Gln Pro Phe Ser Leu Ile Ala Trp Pro 70 ATC TAT TGG GTT CTC CAA GGT TGC CTT CTC ACT GGT GTG TGG GTG ATT 404Ile Tyr Trp Val Leu Gln Gly Cys Leu Leu Thr Gly Val Trp Val Ile 90 GCT CAC GAG TGT GGT CAC CAT GCC TTC AGC AAG TAC CAA TGG GTT GAT Ala His Glu Cys Gly His His Ala Phe Ser Lys Tyr Gln Trp Val Asp 110 GAT GTT GTG GGT TTG ACC CTT CAC TCA ACA CTT TTA GTC CCT TAT TTC 500 Asp Val Val Gly Leu Thr Leu His Ser Thr Leu Leu Val Pro Tyr Phe 120 125 130 TCA TEG AAA ATA AGO CAT CGC CGC CAT CAC TCC AAC ACA GGT TCC CTT Ser Tro Lys Ile Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu 135 140GAC CGT GAT GAA GTG TTT GTC CCA AAA CCA AAA TCC AAA GTT GCA TGG Asp Arg Asp Glu Val Phe Val Pro Lys Pro Lys Ser Lys Val Ala Trp 155 150 TTT TCC AAG TAC TTA AAC AAC CCT CTA GGA AGG GCT GTT TCT CTT CTC Phe Ser Lys Tyr Leu Asn Asr. Pro Leu Gly Arg Ala Val Ser Leu Leu 170 GTC ACA CTC ACA ATA GGG TGG CCT ATG TAT TTA GCC TTC AAT GTC TCT Val Thr Leu Thr Ile Gly Trp Pro Met Tyr Leu Ala Phe Asn Val Ser 195 130 UCD TED TAT TOO DAT DAT DAD DAD AND ITT TOA TAR TAT DOD ADA TROP ory try that The the the the the the the Pro The Ala Pro 200 ر ل ک ATA TAT TOT AAC DET GAG AGE OTT OTG ATO TAT ETC TOT GAT ETT GOT 7 5 3 Ile Tyr Ser Asn Arg Glu Arg Leu Leu Ile Tyr Val Ser Asp Val Ala 215 TTG TTT TGT GTG ACT TAC TGT GTG TAG JGT GTT GGA AGU GTG AAA GGG



GTTATGGAAG TTTTGTGATG TATTAGTACA TAATTAGTAG AATGTTATAA ATAAGTGGAT

TTGCCGCGTA ATGACTTTGT GTGTATTGTG AAACAGCTTG TTGCGATCAT GGTTATAATG 1334

TAAAAATAAT TUTGGTATTA ATTACATGTG GAMAGTGTTI TISTTATAIN TITOTGOOTA

1454

AAAAAAA 1462

- (2) INFORMATION FOR SEQ ID NO:6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (11) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Gly Arg Gly Arg Val Ala Lys Val Glu Val Gln Gly Lys Lys 1 5 10 15

Pro Leu Ser Arg Val Pro Asn Thr Lys Pro Pro Phe Thr Val Gly Gln 20 25 30

Leu Lys Lys Ala Ile Pro Pro His Cys Phe Gln Arg Ser Leu Leu Thr 35 40 45

Ser Phe Ser Tyr Val Val Tyr Asp Leu Ser Phe Ala Phe Ile Phe Tyr 50 55

Ile Ala Thr Thr Tyr Phe His Leu Leu Pro Glr. Pro Phe Ser Leu Ile65707580

Ala Trp Pro Ile Tyr Trp Val Leu Gln Gly Cys Leu Leu Thr Gly Val 85 90 95

Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Lys Tyr Gln

Trp Val Asp Asp Val Val Gly Leu Thr Leu His Ser Thr Leu Leu Val 115 120 125

Pro Tyr Phe Ser Trp Lys Ile Ser His Arg Arg His His Ser Asn Thr 130 135

Gly Ser Leu Asp Ard Asp Glu Val Phe Val Pro Lys Pro Lys Ser Lys 145 - 156 - 160

Via Ald lip the set syl syr sin Air Air, it is usely Arg Ald value 170 175

Ser Leu Leu Val Thr Leu Thr Ile Gly Tro Pro Met Tyr Leu Ala Phe 180 185 190

Asn Val Ser Gly Arg Pro Tyr Asp Ser Phe Ala Ser His Tyr His Pro 195 200 205

Tyr Ala Fro Ilo Tyr Ser Ash Arg Glu Arg Leu Leu Ile Tyr Val Ser

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215 220 210 Asp Val Ala Leu Phe Ser Val Thr Tyr Ser Leu Tyr Arg Val Ala Thr 230 235 Leu Lys Gly Leu Val Trp Leu Leu Cys Val Tyr Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Thr Ile Thr Tyr Leu Gln His Thr His Phe Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly 230 275 Ala Leu Ala Thr Met Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His His Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Asn Ala Ile Lys Pro Ile Leu 330 Gly Glu Tyr Tyr Gln Phe Asp Asp Thr Pro Phe Tyr Lys Ala Leu Trp 340 Ang Glu Ala Ang Glu Cys Leu Tyn Val Glu Pro Asp Glu Gly Thr Ser Glu Lys Gly Val Tyr Trp Tyr Arg Asn Lys Tyr 370 (2) INFORMATION FOR SEQ ID NO:7: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1730 base pairs (B) TYPE: nucle:c acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA HYPOTHETICAL: NO (iii) (IV) ANTI-CENSE: No .v., 201111111 . 10841: (A) ORGANISM: Zea mays

Pau⇔ 14

(B) LOCATION: 165..1328

(B) CLONE: pFad.#1

(ix) FEATURE:
(A) NAME/REY: CDS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGGCCTCTCC CCTCCCTCCT CCCTGCAAAT CCTGCAGACA CCACCGCTCG TTTTTCTCTC 60

CEGGACAGGA GAAAAGGGGA GAGAGAGGTG AGGCGCGGTG TCCGCCCGAT CTGCTCTGCC

degacgeage tettaceace tecteagtet caeteagas caas ats get gee ${\it GGC}$

Met Gly Ala Gly

Gly Arg Met Thr Glu Lys Glu Arg Glu Lys Gln Glu Gln Leu Ala Arg 5 10 15 20

GOT ACC GGT GGC GCC GCG ATG CAG CGG TCG CCG GTG GAG AAG CCT CCG 272

Ala Thr Gly Gly Ala Ala Met Gln Arg Ser Pro Val Glu Lys Pro Pro 25 30 35

TTC ACT CTG GGT CAG ATC AAG AAG GCC ATC CCG CCA CAC TGC TTC GAG $^{\pm\pm\pm}$

Phe Thr New Gly Gln Ile Lys Lys Ala Ile Pro Pro His Cys Phe Glu 41 50

OGO TOG GTG CTC AAG TOC TTC TOG TAC GTG GTC CAC GAC CTG GTG ATC 383

Arg Ser Val Leu Lys Ser Phe Ser Tyr Val Val His Asp Leu Val Ile 55 60 65

300 GCG GCG CTC CTC TAC TTC GCG CTG GCC ATC ATA CCG GCG CTC CCA ± 416 .

Ala Ala Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile Pro Ala Leu Pro 70 75 30

AGO COG CTC CGC TAC GCC GCC TGG CCG CTG TAC TGG ATC GCG CAG GGG

Ser Pro Leu Arg Tyr Ala Ala Trp Pro Leu Tyr Trp Ile Ala Gln Gly -85 90 95 100

TO STOR THE ACT SEC STE THE STE ATT GOS CAC HAS THE GIG CAC HAS

Cys Val Cys The Gry Val Tro Val Ilo Ala Hiz blu Cyc Gly His His

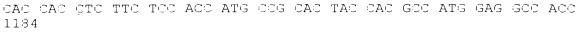
GOU TTO TUG GAO FAC FOR OTO OTS GAO GAO GTG GTO GGO OTS GTG OTS.

Ala Phe Ser Asp Tyr Ser Led Led Asp Asp Val Val Gly Led Val Led 125

CAC TOS TOS OTO ATS STG COO TAC TTO TOS TGS AAS TAC AGO CAD OGG

His Ger Ser Lea Met Val Fro Tyr Phe Ser Trp Lys Tyr Ser His Aig

		135					140					145			
CGC CA 656	ĄC	CAC	TCC	AAC	ACG	GGG	TCC	CTG	GAG	CGC	GAC	GAG	GTG	TTC	GTG
Arg Hi	is 50	His	Ser	Asn	Thr	Gly 155	Ser	Leu	Glu	Arg	Asp 160	Glu	Val	Phe	Val
CCC AF	ĄG	AAG	AAG	GAG	GCG	CTG	CCG	TGG	TAC	ACC	CCG	TAC	GTG	TAC	AAC
Pro Ly 165	/S	Lys	Lys	Glu	Ala 170	Leu	Pro	Trp	Tyr	Thr 175	Pro	Tyr	Val	Tyr	Asn 180
AAC CC 752	CG	GTC	GGC	CGG	GTG	GTG	CAC	ATC	GTG	GTG	CAG	CTC	ACC	CTC	GGG
Asn Fi	ro	Val	Gly	Arg 185	Val	Val	His	Ile	Val 190	Val	Gln	Leu	Thr	Leu 195	Gly
TGG C0	CG	ÇTG	TAC	CTG	GCG	ACC	AAC	GCG	TCG	GGG	CGG	CCG	TAC	CCG	CGC
Trp Pi	ro	Leu	Tyr 200	Leu	Ala	Thr	Asn	Ala 205	Ser	Gly	Arg	Pro	Tyr 210	Pro	Arg
TTC G0	CC	TGC	CAC	TTC	GAC	CCC	TAC	GGC	CCC	ATC	TAC	AAC	GAC	CGG	GAG
Phe Al	l-à	Cys 215	His	Fhe	Asp	Pro	Tyr 220	Gly	Pro	Il⊖	Tyr	Asn 225	Asp	Arg	Glu
CGC G0	20	CAG	ATC	TTC	GTC	TCG	GAC	GCC	GGC	GTC	GTG	GCC	GTG	GCG	TTC
Arg Al	La 30	Gln	Ile	Fhe	Val	Ser 235	Asp	Ala	Gly	Va l.	Val 240	Ala	Val	Ala	Phe
GGG 07	ГG	TAC	AAG	CTG	GCG	GCG	GCG	TTC	GGG	GTC	TGG	TGG	GTG	GTG	CGC
Gly Le 245	∋u	Tyr	Lys	Leu	Ala 250	Ala	Ala	Phe	Gly	Val 255	Trp	Trp	Val	Val	Arg 260
GTG TA	AC.	GCC	GTG	CCG	CTG	CTG	ATC	GTG	AAC	GCG	TGG	CTG	GTG	CTC	ATC
Val Ty	r	Ala		Pro 265		Leu	Ile		Asn 270		Trp	Leu	Val	Leu 275	
ACC TA	A.C	CTG	CAG	CAC	ACC	CAC	CCG	TCG	CTC	CCC	CAC	TAC	GAC	TCG	AGC
Thr Ty	'nr	Leu	Gin 280	His	Tnr	ніз	Fric	Ser 235	Leu	Fro	Hıs	Гуr	Asp 291	Ser	Ser
GAG T0	717	GAC	TGG	· T:G	iC(GiC	GGC	FiC in	CTB	GCT	ACC	ATG	GAC	CGC	GAC	ГАС
Glu Tı	rp	Asp 295	Trp	Leu	Arg	Gly	A1a 300	Leu	Ala	Thr	Met	Asp 305	Arg	Asp	Tyr
GGC A:	rc	CTC	AAC	CGC	GTG	TTC	CAC	AAC	ATC	ACG	GAC	ACG	CAC	GTC	GCG
Gly I	le 10	Leu	Asn	Arg	Val	Phe 315	His	Asr.	Ile	Thr	Asp 320	Thr	His	Val	Ala



His His Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr 325 330 335 340

AAG GCG ATC AGG CCC ATC CTC GGC GAC TAC TAC CAC TTC GAC CCG ACC 1232

Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Pro Thr 345 350 355

CCT GTC GCC AAG GCG ACC TGG CGC GAG GCC GGG GAA TGC ATC TAC GTC 1280 $\,$

Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu Cys Ile Tyr Val 360 365 370

GAG COC GAG GAC CGC AAG GGC GTC TTC TGG TAC AAG AAG AAG TTC TAGCCGCCG C 1335

Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn Lys Lys Phe 375 380 385

CGCTCGCAGA GCTGAGGACG CTACCGTAGG AATGGGAGCA GAAACCAGGA GGAGGAGACG 1395

STACTOSCOC CAAAGTOTOO GTCAACOTAT CTAATOGTTA GTCGTCAGTC TTTTAGACGG 1455

GAAGAGAGAT CATTTGGGCA CAGAGACGAA GGCTTACTGC AGTGCCATCG CTAGAGCTGC 1515

CATCAAGTAC AAGTAGGCAA ATTCGTCAAC TTAGTGTGTC CCATGTTGTT TTTCTTAGTC

GTCCGCTGCT GTAGGCTTTC CGGCGGCGGT CGTTTGTGTG GTTGGCATCC GTGGCCATGC

CTGTGDGTGC GTGGCCGCGC TTGTCGTGTG CGTCTGTCGT CGCGTTGGCG TCGTCTCTTC

GTGCTCCCCG TGTGTTGTTG TAAAACAAGA AGATGTTTTC TGGTGTCTTT GGCGGAATAA 1755

CAGATCGTCC GAACGAAAAA AAAAAAAAAA AAAAA 1790

- (2) INFORMATION FOR SEQ ID NO:8:
 - 1 (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGIH: 38% amino adida
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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Met Gly Ala Gly Gly Arg Met Thr Glu Lys Glu Arg Glu Lys Gln Glu Gln Leu Ala Arg Ala Thr Gly Gly Ala Ala Met Gln Arg Ser Pro Val Glu Lys Pro Pro Phe Thr Leu Gly Gln Ile Lys Lys Ala Ile Pro Pro His Cys Phe Glu Arg Ser Val Lou Lys Ser Phe Ser Tyr Val Val His Asp Leu Val Ile Ala Ala Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile Pro Ala Leu Pro Ser Pro Leu Arg Tyr Ala Ala Trp Pro Leu Tyr Trp Ile Ala Gln Gly Cys Val Cys Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp Val Val 115 Gly Leu Val Leu His Ser Ser Lou Met Val Pro Tyr Phe Ser Trp Lys 1.35 Tyr Ser His Arg Arg His His Ser Ash Thr Gly Ser Leu Glu Arg Asp Gia Val Phe Val Pro Lys Lys Giu Ala Leu Pro Trp Tyr Thr Pro Tyr Val Tyr Asr. Asn Pro Val Gly Arg Val Val His Ile Val Val Gln 185 Leu Thr Leu Gly Trp Pro Leu Tyr Leu Ala Thr Ash Ala Ser Gly Arg 195 $$20^{\circ}$$ Pro Tyr Pro Ang Phe Ala Cys His Phe Asp Pro Tyr Gly Pro Ile Tyr Ash Asp Arg Glu Arg Ala Gln fle Phe Val Ser Asp Ala Gly Val Val A a Val Ala Phe Glv Lew Tvr Low Low Ala Ala Ala Pho Gly Val Trp Trp Val Val Arg Val Tyr Ala Va. Fro Leu Leu Ile Val Ast Ala Trp 260 Leu Val Leu Ile Thr Tyr Lou Si: His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Met

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Asp Arg Asp Tyr Gly Ile Leu Asn Arg Val Phe His Asn Ile Thr Asp 305 310 315 320

Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala 325 330 335

Met Glu Ala Thr Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His 340 345 350

Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu 355 360 365

Cys Ile Tyr Val Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn 370 375 380

Lys Lys Phe 335

- (2) INFORMATION FOR SEC ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 673 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) OF.GANISM: Ficinus communis
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: pRF2-10
 - (ix) FEATURE:
 - (A) NAME/REY: CDS
 - (B) LOCATION: 1..673
 - /yi' decurred besoriemion: SEO ID NO:9:

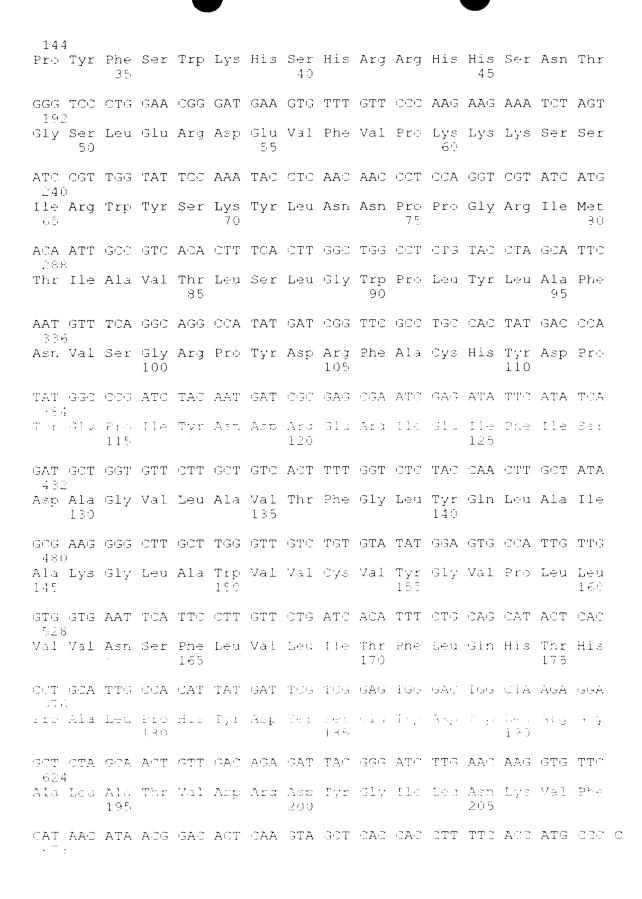
THE OTHER PROCESS OF THE STATE THE GREEN CAN GAT GOOD THE AGT GAS TAT CAA 48

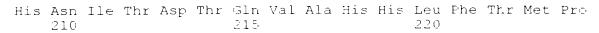
The Mark The Min Bop Che Cly His His Bla Phe Ser Asp Tyr Gln

1 15

TTG CTT GAT GAT GTA GTT GGT CTT ATC CTA CAC TCC TGT CTC CTT GTC 96 Leu Leu Asp Asp Val Val Gly Leu Ile Leu His Ser Cys Leu Leu Val

COT TAT TIT TOA TGG AAA CAS AGS CAT SGC SGA SAT SAT TOS AAS ASA





- (2) INFORMATION FOR SEQ ID NO:10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His Ser Asn Thr 35 40 45

Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Ser Ser 50 55 60

Ile Arg Trp Tyr Ser Lys Tyr Neu Ash Ash Pro Pro Gly Arg Ile Met 65 /5 /5 80

Thr Ile Ala Val Thr Leu Ser Leu Gly Trp Pro Leu Tyr Leu Ala Phe 95 99 95

Ash Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr Asp Pro 100 105 110

Tyr Gly Pro Ile Tyr Asr. Asp Arg Glu Arg Ile Glu Ile Phe Ile Ser 115 120 125

Asp Ala Gly Val Leu Ala Val Thr Phe Gly Leu Tyr Gln Leu Ala Ile 130 135 140

Ala Eys Gly Leu Ala Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu 145 - 155 - 160

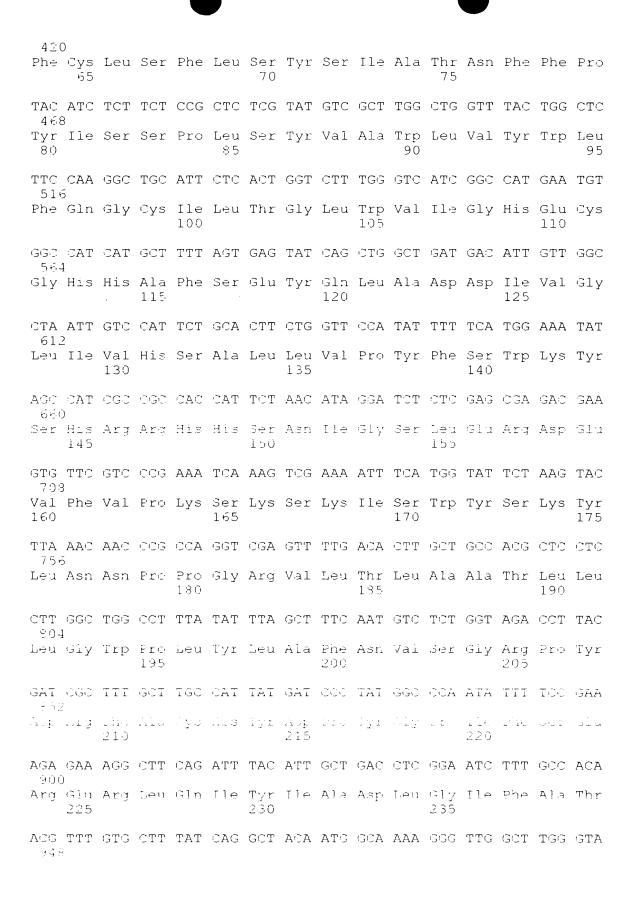
Val Val Asr. Ser Ene Lou Val Beu The Thr Phe Leu Gin His Thr His 185 - 175

Pro Ala Leu Pro His Tyr Asp Ser Ser Glu Tro Asp Trp Leu Ard Gly
180 180

Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe 195 200 205

His Asn Ile Thr Asp Thr Gln Val Ala His His Leu Phe Thr Met Pro 210 215 220

- (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) OFGANISM: Ricinus communis
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: pRF197c-42
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 184..1347
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
- CGGCCGGGAT TCCGGTTTTC ACACTAATTT CCAAAAAATG CATGATTTCA CCTCAAATCA
- AACACCACAC CTTATAACTT AGTCTTAAGA GAGAGAGAGA GAGGAGACAT TTCTCTCTCTC
- TGAGATGAGC ACTTCTCTTC CAGACATCGA AGCCTCAGGA AAGTGCTTGA GAAGAGCTTG
- AGA ATG GGA GGT GGT GGC ATG TOT ACT GTC ATA ATC AGC AAC AAC
 - Met Gly Gly Gly Ard Met Ser Thr Val Ile Ile Ser Asn Asn 1 5 10 15
- AGT GAG AAG AAA EGA EGA AGC AGC CAC CTG GAG CGA GCG CCG CAC ACG
- Ser Glu Lys Lys Gly Gly Ser Ser His Leu Glu Arg Ala Pro His Thr 20 25 30
- ARG COT COT TAC ACA OFF BGF ARG OFG ARG AGA GOO ATO COA COO CAF
- Lvs Pro Pro Tvr Tnr Leu Gly Ash Leu Lys Ard Ala Ile Pro Pro His
- TGG TTT SAA CGG TGT TTT GTG CGG TGA TTG TGG AAT TTT GCC TAT AAT $^{3.79}$
- Cys Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Asn Phe Ala Tyr Asn 50 55 60
- TTO TGO TTA AGT TIT CTT TOO TAG TIG ATO GOO AGO AAC TTO TTO COT



Thr Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val 245 250 ATG CGT ATC TAT GGG GTG CCA TTG CTT ATT GTT AAC TGT TTC CTT GTT Met Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val 265 260 ATG ATC ACA TAC TTG CAG CAC ACT CAC CCA GCT ATT CCA CGC TAT GGC 1044 Met Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly 285 280 275 TCA TCG GAA TGG GAT TGG CTC CGG GGA GCA ATG GTG ACT GTC GAT AGA 1092Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg 290 295 GAT TAT GGG GTG TTG AAT AAA GTA TTC CAT AAC ATT GCA GAC ACT CAT 1140 Asp Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His 310 305 GTA GCT CAT CAT CTC TTT GCT ACA GTG CCA CAT TAC CAT GCA ATG GAG 1138 Val Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu 330 GCC ACT AAA GCA ATC AAG CCT ATA ATG GGT GAG TAT TAC CGG TAT GAT Ala Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp 340 GGT ACC CCA TTT TAC AAG GCA TTG TGG AGG GAG GCA AAG GAG TGC TTG 1284 Gly Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu 355 360 TTO GTO GAG COA GAT GAA GGA GOT COT ACA CAA GGO GTT TTO TGG TAC 1332 Phe Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr 375 370 CGG AAC AAG TAT TAAAAAAGTG TCATGTAGCC TGCCG エろもヲ

.2. INFORMATION FOR SEQ ID No:12:

Arg Asn Lys Ty:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 387 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- dii Molecule Type: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: Met Gly Gly Gly Arg Met Ser Thr Val Ile Ile Ser Asn Asn Ser 1.0 Glu Lys Lys Gly Gly Ser Ser His Leu Glu Arg Ala Pro His Thr Lys Pro Pro Tyr Thr Leu Gly Asn Leu Lys Arg Ala Ile Pro Pro His Cys Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Ash Phe Ala Tyr Ash Phe Cys Leu Ser Phe Leu Ser Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly 100 His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Leu 170Ash Ash Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu Gly Trp Pro Leu Tyr Leu Ala Phe Ash Val Ser Gly Arg Pro Tyr Asp 200 Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg The four Time Ile Turn the Ala The Ten Gly I.e The Ala The The 200 200 Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met 245 Arg Ile Tyr Jly Val Pro Leu Leu Ile Val As.. Cy: The Lou Val Met Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser 280

Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp 295 Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val 315 Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly 340 345 350 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe

Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg 380

Asn Lys Tyr 385

INFORMATION FOR SEQ ID NO:13: (2)

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
- TYPE: nucleic arid
- STRAMBEDMESS: single (C)
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
- (A) NAME/REY: misc_feature(B) LOCATION: 1..23
- (D) OTHER INFORMATION: /product=

"synthetic

TOCOTATIONS TO WITH ME AND AND AND

oligonucleotide"

"xi" ENPURME DESCRIPTION: SEQ ID NO:13:

23

- (1) SEQUINCE CHAPACTERISTICS:
- (A) LENGTH: 22 base pairs

- (E) TYPE: nucleic acid
- (C) TRANDEDNESS: single
- (D) TOPOLOGY: linear
- (11) MCLECULE TYPE: CDNA

Dage 26

(iii) HYPOTHETICAL: NO

	(iv)	ANTI-SI	ense: No				
	(A) NAI (B) LO	CATION: HER INFO tic	misc_fea 122 ORMATION:	ture /product=			
	(xi)	SEQUEN	CE DESCRIE	TION: SEQ) ID NO:14:		
AAARTGRI	rgg cacr	TGNGTR '	TC			22	
(2)	INFORMA	TION FO	R SEQ ID N	10:15:			
	(A) LE: (E) TY (C) ST:	NGTH: . PE: nu RANDEDNI	CE CHARACT 2973 base cleic acid ESS: doub linear	pairs			
	(ii)	MOLECU	LE TYPE:	DNA (genom	iic)		
	(111)	interior	Eulinavit.• β	ĮO.			
	(iv)	ANTI-SI	ENSE: NO				
			AL SOURCE: Arabidop	sis thalia	ına		
	(vii) (F) CL		ATE SOUPCE AGF2-6	: :			
	(A) NAI)			
		ME/KEY:	E: intron 521165	5.4			
	(xi)	SEQUEN	OF DESCRIF	PTION: SEQ	ID NO:15:		
ATTCGGT <i>i</i>	AAT TOUT.	ACATAT :	TTTAGAGAT"I	. AGTTTGAGT	T 100.VICCA	IA UTTTAMAG	
gattataa 20	AAT TTML	AATAD9 1	TACUTTUO BA	CTATAAAGI	G AAACTAAG	IA AATTAGAACG	5 1
TGATATTA 80	AAA AAGT	TAATGT	TCACTGTTAT	ATTTTTTT	CA CAAGTAAA.	AA ATGGGTTATT	. 1
TGCGGTAA	AAAA TAA	ATACCA	GATATTTTGA	A ATTGATTAA	a aaggttga	AA TAAGAGAGGA	À 2

40

GGGGAAAGAA 00	AAGAAGGTGG	GGGCCCAGTA	TGAAAGGGAA	AGGTGTCATC	AAATCATCTC	3
TCTCTCTCTC 60	TACCTTCGAC	CCACGGGCCG	TGTCCATTTA	AAGCCCTGTC	TCTTGCCATT	3
CCCCATCTGA 20	CCACCAGAAG	AAGAGCCACA	CACTCACAAA	TTAAAAAGAG	AGAGAGAGAG	1
AGAGAGACAG 80	AGAGAGAGAG	AGATTOTGCG	GAGGAGCTTC	TTCTTCGTAG	GGTGTTCATC	4
GTTATTAACG 40	TTATCGCCCC	TACGTCAGCT	CCATCTCCAG	GTCCGTCGCT	TCTCTTCCAT	5
TTCTTCTCAT	TTTCGATTTT	GATTCTTATT	TCTTTCCAGT	AGCTCCTGCT	CTGTGAATTT	ŧō
CTCCGCTCAC 60	GATAGATCTG	CTTATACTCC	TTACATTCAA	CCTTAGATCT	GGTCTCGATT	6
CTCTGTTTCT	CTGTTTTTTT	CTTTTGGTCG	AGAATCTGAT	GTTTGTTTAT	GTTCTGTCAC	7
CATTAATAAT 80	CVACAY A Laborit	CICATICATA	CAATGATTAG	TTTCTCTCGT	CTACCAAACG	,
ATATGTTGCA 40	TTTTCACTTT	TCTTCTTTTT	TTCTAAGATG	ATTTGCTTTG	ACCAATTTGT	8
TTAGATCTTT U0	ATTTTATTTT	ATTTTCTGGT	GGGTTGGTGG	AAATTGAAAA	AAAAAAAA	Ģ
AAAAGCATAA 60	ATTGTTATTT	GTTAATGTAT	TCATTTTTTG	GCTATTTGTT	CTGGGTAAAA	g,
ATCTGCTTCT	ACTGTTGAAT	CTTTCCTGGA	TTTTTTACTC	CTATTGGGTT	TTTATAGTAA	10
AAATACATAA RO	TAAAAGGAAA	ACAAAAGTTT	TATAGATTCT	CTTAAACCCC	TTACGATAAA	10
AGTTGGAATC	AAAATAATTO	AGGATCAGAT	GCTCTTTGAT	TGATTCAGAT	GCGATTACAG	i i
ora Emilyak indukiy	VVALALACAVO.	Ymcocarcano	ΔοΑπήψηΑήτ	тџстаттрАА	ATATCTAAAT	1.2
CTGATATATG	ATGTCGACAA	ATTCTGGTGG	CTTATACATC	ACTTCAACTG	TTTTCTTTTG	12
GCTTTGTTTG 20	TCAACTTGGT	TTTCAATACS	ATTTGT GATT	TOGATOGOTG	AATTTTTAAT	13

ACAAGCAAAC 80	TGATGTTAAC	CACAAGCAAG	AGATGTGACC	TGCCTTATTA	ACATOGTATT	13
ACTTACTACT 40	AGTOGTATTO	TCAACGCAAT	CGTTTTTGTA	TTTCTCACAT	TATGCCGCTT	14
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reassmasee eu	CTTGTACTTA	GCCTTTAACC	TOTOTOGICAG	AUCGTAT SAU	GGGTTOGUIT	
GCCAFTTCTT	JUCJAAUGUT	JUCATOTACA	AT SACCGAGA	ADGCCTCCAG	APATALOTUI	5
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TCCACAAC	CAT TACAGACACA	CACGTGGCTC	ATCACCTGTT	CTCGACAATG	CCGCATTATA	.26		
ACGCAATO	GGA AGCTACAAAG	GCGATAAAGC	CAATTCTGGG	AGACTATTAC	CAGTTCGATG	27		
GAACACCC	STG GTATGTGGCG	ATGTATAGGG	AGGCAAAGGA	GTGTATCTAT	GTAGAACCGG	27		
ACAGGGAA 20	AGG TGACAAGAAA	GGTGTGTACT	GGTACAACAA	TAAGTTATGA	GGATGATGGT	.:8		
GAAGAAAT 80	TTG TOGACTTTTC	TCTTGTCTGT	TTGTCTTTTG	TTAAAGAAGC	TATGCTTCGT	28		
TTTAATAA	ATC TTATTGTCCA	TTTTGTTGTG	TTATGACATT	TTGGCTGCTC	ATTATGTTAT	.19		
GTGGGAAG	STT AGCGTTCAAA	TGTTTTGGGGT	agg			29		
(2)	INFORMATION F	OR SEQ ID NO	0:16:					
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 23 base pairs(B) TYPE: nucleic acid(C) STEANDEDNESS: single(D) TOPOLOGY: linear							
	(ii) MOLEC	ULE TYPE: .	CDNA					
	(iii) HYPOT	HETICAL: No	D)					
	-ITMA (vi)	SENSE: NO						
	(ix) FEATU (A) NAME MEY (B) LOCATION (II) OTHER TN "Syntheria" (Cliropuolinti	: miso fear : 123 RORMATION:						
	(xi) SEQUE	MOE DESCRIP	rion: SEQ I	ID NO:16:				
GGGUATGT	INU ARAANAERTG	FTG		23				
(2)	INFORMATION F	OR SEQ ID N	0:17:					

i: SEQUENCE THARACTERISTICS:

- (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..23
 (D) OTHER INFORMATION: /product=
- "synthetic
- oligonuclectide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGCATGTRC TRAANAERTG ETG

23